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Date of Deposit: December 5, 2001

Docket No.: 15966-559 CON-S6 (Cura-59 CON-S6)

**IN THE UNITED STATES PATENT AND TRADEMARK OFFICE**

FIRST-NAMED INVENTOR: Shimkets

FOR: Novel Amino Acid Sequences For Human Fetal Brain-like Polypeptides

JC760 U.S. PTO  
10/004551  
12/05/01

Assistant Commissioner for Patents  
Washington, D.C. 20231

**REQUEST FOR TRANSFER OF SEQUENCE LISTING UNDER 37 C.F.R. § 1.821(e)**

The computer readable copy of the Sequence Listing in the instant application is identical to the sequence information in the computer readable copy of the sequence listing filed in application 09/635,949, filed August 10, 2000. In accordance with 37 C.F.R. §1.821(e), please use only the computer readable form in application 09/635,949 as the computer readable form for the instant application. It is understood that the Patent and Trademark Office will make the necessary change in the application number, applicants and filing date for the instant application.

A paper copy of the Sequence Listing was included in the originally filed specification of the earliest priority application, application number 09/635,949 filed August 10, 2000. Please use only the paper copy of the Sequence listing of this application as the paper copy for the instant application.

Respectfully submitted,

Dated: December 5, 2001

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Ivor R. Elrifī, Reg. No. 39,529  
Naomi S. Biswas, Reg. No. 38,384  
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One Financial Center  
Boston, Massachusetts 02111  
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## SEQUENCE LISTING

<110> SHIMKETS, RICHARD A  
FERNANDES, ELMA

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<141> 2000-08-10

*9/30/03*  
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355                    360                    365

Thr Pro Leu His Gln Leu Tyr Ser Ala Ala Phe Ser Lys Gln Lys Leu  
370                    375                    380

Gln Ser Ala Pro Thr Lys Lys Pro Ala Leu Pro Phe Gly Asp Leu Pro  
385                    390                    395                    400

Met Gly Tyr Gln His Leu His Thr Gln Leu Gln Tyr Glu Cys Ile Ser  
405                    410                    415

Pro Phe Tyr Arg Arg Leu Gly Ser Ser Arg Lys Thr Cys Leu Lys Thr  
420                    425                    430

Gly Lys Trp Ser Gly Arg Ala Pro Ser Cys Ile Pro Ile Cys Gly Lys

435

440

445

Ile Glu Asn Ile Thr Ala Pro Lys Thr Gln Gly Leu Arg Trp Pro Trp

450

455

460

Gln Ala Ala Ile Tyr Arg Arg Thr Ser Gly Val His Asp Gly Ser Leu

465

470

475

480

His Lys Gly Ala Trp Phe Leu Val Cys Ser Gly Ala Leu Val Asn Glu

485

490

495

Arg Thr Val Val Val Ala Ala His Cys Val Thr Asp Leu Gly Lys Val

500

505

510

Thr Met Ile Lys Thr Ala Asp Leu Lys Val Val Leu Gly Lys Phe Tyr

515

520

525

Arg Asp Asp Asp Arg Asp Glu Lys Thr Ile Gln Ser Leu Gln Ile Ser

530

535

540

Ala Ile Ile Leu His Pro Asn Tyr Asp Pro Ile Leu Leu Asp Ala Asp

545

550

555

560

Ile Ala Ile Leu Lys Leu Leu Asp Lys Ala Arg Ile Ser Thr Arg Val

565

570

575

Gln Pro Ile Cys Leu Ala Ala Ser Arg Asp Leu Ser Thr Ser Phe Gln

580

585

590

Glu Ser His Ile Thr Val Ala Gly Trp Asn Val Leu Ala Asp Val Arg

595

600

605

Ser Pro Gly Phe Lys Asn Asp Thr Leu Arg Ser Gly Val Val Ser Val

610

615

620

Val Asp Ser Leu Leu Cys Glu Glu Gln His Glu Asp His Gly Ile Pro

625

630

635

640

Val Ser Val Thr Asp Asn Met Phe Cys Ala Ser Trp Glu Pro Thr Ala

645

650

655

Pro Ser Asp Ile Cys Thr Ala Glu Thr Gly Gly Ile Ala Ala Val Ser

660

665

670

Phe Pro Gly Arg Ala Ser Pro Glu Pro Arg Trp His Leu Met Gly Leu

675

680

685

Val Ser Trp Ser Tyr Asp Lys Thr Cys Ser His Arg Leu Ser Thr Ala

690

695

700

Phe Thr Lys Val Leu Pro Phe Lys Asp Trp Ile Glu Arg Asn Met Lys

705

710

715

720



cca aag tat gta aaa gag tta cat ttg caa gaa aat aac ata agg act 811  
Pro Lys Tyr Val Lys Glu Leu His Leu Gln Glu Asn Asn Ile Arg Thr  
105 110 115

atc act tat gat tca ctt tca aaa att ccc tat ctg gaa gaa tta cat 859  
Ile Thr Tyr Asp Ser Leu Ser Lys Ile Pro Tyr Leu Glu Glu Leu His  
120 125 130

tta gat gac aac tct gtc tct gca gtt agc ata gaa gag gga gca ttc 907  
Leu Asp Asp Asn Ser Val Ser Ala Val Ser Ile Glu Glu Gly Ala Phe  
135 140 145 150

cga gac agc aac tat ctc cga ctg ctt ttc ctg tcc cgt aat cac ctt 955  
Arg Asp Ser Asn Tyr Leu Arg Leu Leu Phe Leu Ser Arg Asn His Leu  
155 160 165

agc aca att ccc tgg ggt ttg ccc agg act ata gaa gaa cta cgc ttg 1003  
Ser Thr Ile Pro Trp Gly Leu Pro Arg Thr Ile Glu Glu Leu Arg Leu  
170 175 180

gat gat aat cgc ata tcc act att tca tca cca tct ctt caa ggt ctc 1051  
Asp Asp Asn Arg Ile Ser Thr Ile Ser Ser Pro Ser Leu Gln Gly Leu  
185 190 195

act agt cta aaa cgc ctg gtt cta gat gga aac ctg ttg aac aat cat 1099  
Thr Ser Leu Lys Arg Leu Val Leu Asp Gly Asn Leu Leu Asn Asn His  
200 205 210

ggt tta ggt gac aaa gtt ttc ttc aac cta gtt aat ttg aca gag ctg 1147  
Gly Leu Gly Asp Lys Val Phe Phe Asn Leu Val Asn Leu Thr Glu Leu  
215 220 225 230

tcc ctg gtg cggtt aat tcc ctg act gct gca cca gta aac ctt cca ggc 1195  
Ser Leu Val Arg Asn Ser Leu Thr Ala Ala Pro Val Asn Leu Pro Gly  
235 240 245

aca aac ctg agg aag ctt tat ctt caa gat aac cac atc aat cggt 1243  
Thr Asn Leu Arg Lys Leu Tyr Leu Gln Asp Asn His Ile Asn Arg Val  
250 255 260

ccc cca aat gct ttt tct tat cta agg cag ctc tat cga ctg gat atg 1291  
Pro Pro Asn Ala Phe Ser Tyr Leu Arg Gln Leu Tyr Arg Leu Asp Met  
265 270 275

tcc aat aat aac cta agt aat tta cct cag ggt atc ttt gat gat ttg 1339  
Ser Asn Asn Asn Leu Ser Asn Leu Pro Gln Gly Ile Phe Asp Asp Leu  
280 285 290

gac aat ata aca caa ctg att ctt cgc aac aat ccc tgg tat tgc ggg 1387  
Asp Asn Ile Thr Gln Leu Ile Leu Arg Asn Asn Pro Trp Tyr Cys Gly  
295 300 305 310

tgc aag atg aaa tgg gta cgt gac tgg tta caa tca cta cct gtg aag 1435  
Cys Lys Met Lys Trp Val Arg Asp Trp Leu Gln Ser Leu Pro Val Lys  
315 320 325

gtc aac gtg cgt ggg ctc atg tgc caa gcc cca gaa aag gtt cgt ggg 1483  
Val Asn Val Arg Gly Leu Met Cys Gln Ala Pro Glu Lys Val Arg Gly  
330 335 340

atg gct att aag gat ctc aat gca gaa ctg ttt gat tgt aag gac agt 1531  
Met Ala Ile Lys Asp Leu Asn Ala Glu Leu Phe Asp Cys Lys Asp Ser  
345 350 355

ggg att gta agc acc att cag ata acc act gca ata ccc aac aca gtg 1579  
Gly Ile Val Ser Thr Ile Gln Ile Thr Thr Ala Ile Pro Asn Thr Val  
360 365 370

tat cct gcc caa gga cag tgg cca gct cca gtg acc aaa cag cca gat 1627  
Tyr Pro Ala Gln Gly Gln Trp Pro Ala Pro Val Thr Lys Gln Pro Asp  
375 380 385 390

att aag aac ccc aag ctc act aag gat caa caa acc aca ggg agt ccc 1675  
Ile Lys Asn Pro Lys Leu Thr Lys Asp Gln Gln Thr Thr Gly Ser Pro  
395 400 405

tca aga aaa aca att aca att act gtg aag tct gtc acc tct gat acc 1723  
Ser Arg Lys Thr Ile Thr Ile Thr Val Lys Ser Val Thr Ser Asp Thr  
410 415 420

att cat atc tct tgg aaa ctt gct cta cct atg act gct ttg aga ctc 1771  
Ile His Ile Ser Trp Lys Leu Ala Leu Pro Met Thr Ala Leu Arg Leu  
425 430 435

agc tgg ctt aaa ctg ggc cat agc ccg gca ttt gga tct ata aca gaa 1819  
Ser Trp Leu Lys Leu Gly His Ser Pro Ala Phe Gly Ser Ile Thr Glu  
440 445 450

aca att gta aca ggg gaa cgc agt gag tac ttg gtc aca gcc ctg gag 1867  
Thr Ile Val Thr Gly Glu Arg Ser Glu Tyr Leu Val Thr Ala Leu Glu  
455 460 465 470

cct gat tca ccc tat aaa gta tgc atg gtt ccc atg gaa acc agc aac 1915  
Pro Asp Ser Pro Tyr Lys Val Cys Met Val Pro Met Glu Thr Ser Asn  
475 480 485

ctc tac cta ttt gat gaa act cct gtt tgt att gag act gaa act gca 1963  
Leu Tyr Leu Phe Asp Glu Thr Pro Val Cys Ile Glu Thr Glu Thr Ala  
490 495 500

ccc ctt cga atg tac aac cct aca acc acc ctc aat cga gag caa gag 2011  
Pro Leu Arg Met Tyr Asn Pro Thr Thr Thr Leu Asn Arg Glu Gln Glu  
505 510 515

aaa gaa cct tac aaa aac ccc aat tta cct ttg gct gcc atc att ggt 2059

Lys Glu Pro Tyr Lys Asn Pro Asn Leu Pro Leu Ala Ala Ile Ile Gly  
520 525 530

ggg gct gtg gcc ctg gtt acc att gcc ctt ctt gct tta gtg tgt tgg 2107  
Gly Ala Val Ala Leu Val Thr Ile Ala Leu Leu Ala Leu Val Cys Trp  
535 540 545 550

tat gtt cat agg aat gga tcg ctc ttc tca agg aac tgt gca tat agc 2155  
Tyr Val His Arg Asn Gly Ser Leu Phe Ser Arg Asn Cys Ala Tyr Ser  
555 560 565

aaa ggg agg aga aga aag gat gac tat gca gaa gct ggc act aag aag 2203  
Lys Gly Arg Arg Arg Lys Asp Asp Tyr Ala Glu Ala Gly Thr Lys Lys  
570 575 580

gac aac tct atc ctg gaa atc agg gaa act tct ttt cag atg tta cca 2251  
Asp Asn Ser Ile Leu Glu Ile Arg Glu Thr Ser Phe Gln Met Leu Pro  
585 590 595

ata agc aat gaa ccc atc tcg aag gag gag ttt gta ata cac acc ata 2299  
Ile Ser Asn Glu Pro Ile Ser Lys Glu Glu Phe Val Ile His Thr Ile  
600 605 610

ttt cct cct aat gga atg aat ctg tac aaa aac aat cac agt gaa agc 2347  
Phe Pro Pro Asn Gly Met Asn Leu Tyr Lys Asn Asn His Ser Glu Ser  
615 620 625 630

agt agt aac cga agc tac aga gac agt ggt att cca gac tca gat cac 2395  
Ser Ser Asn Arg Ser Tyr Arg Asp Ser Gly Ile Pro Asp Ser Asp His  
635 640 645

tca cac tca tgatgctgaa ggactcacag cagacttg tttgggltt 2444  
Ser His Ser

ttaaaccta agggaggtga tggtaggaac cctgttctac tgcaaaacac tggaaaaaga 2504

gactgaaaaa aagcaatgt atgtacattt gccataataat ttatattaa gaactttta 2564

ttaaaagttt caaatttcag gttactgctg cgattgtatgt agtggagatg cctgaacaca 2624

attctatattt ttagtattttt tttagtaattt gtactgtattt ttcccttgcaa atattggagt 2684

tataaaccat ttacttttg tttctactgag taagatgact ttttgactgt gaaagtgaat 2744

tttcttgctg tgtcgacaa tcaggactgc attcatatga gatcctgtatgt gataaggcac 2804

aggccatttt tcacttttgtt attaataaaaaa tgtaaaaaaaaaaa aaaltgg 2852

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<211> 649  
<212> PRT  
<213> Homo sapiens

<400> 6

Met Ile Ser Ala Ala Trp Ser Ile Phe Leu Ile Gly Thr Lys Ile Gly  
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Leu Phe Leu Gln Val Ala Pro Leu Ser Val Met Ala Lys Ser Cys Pro  
20 25 30

Ser Val Cys Arg Cys Asp Ala Gly Phe Ile Tyr Cys Asn Asp Arg Phe  
35 40 45

Leu Thr Ser Ile Pro Thr Gly Ile Pro Glu Asp Ala Thr Thr Leu Tyr  
50 55 60

Leu Gln Asn Asn Gln Ile Asn Asn Ala Gly Ile Pro Ser Asp Leu Lys  
65 70 75 80

Asn Leu Leu Lys Val Glu Arg Ile Tyr Leu Tyr His Asn Ser Leu Asp  
85 90 95

Glu Phe Pro Thr Asn Leu Pro Lys Tyr Val Lys Glu Leu His Leu Gln  
100 105 110

Glu Asn Asn Ile Arg Thr Ile Thr Tyr Asp Ser Leu Ser Lys Ile Pro  
115 120 125

Tyr Leu Glu Glu Leu His Leu Asp Asp Asn Ser Val Ser Ala Val Ser  
130 135 140

Ile Glu Glu Gly Ala Phe Arg Asp Ser Asn Tyr Leu Arg Leu Leu Phe  
145 150 155 160

Leu Ser Arg Asn His Leu Ser Thr Ile Pro Trp Gly Leu Pro Arg Thr  
165 170 175

Ile Glu Glu Leu Arg Leu Asp Asp Asn Arg Ile Ser Thr Ile Ser Ser  
180 185 190

Pro Ser Leu Gln Gly Leu Thr Ser Leu Lys Arg Leu Val Leu Asp Gly  
195 200 205

Asn Leu Leu Asn Asn His Gly Leu Gly Asp Lys Val Phe Phe Asn Leu  
210 215 220

Val Asn Leu Thr Glu Leu Ser Leu Val Arg Asn Ser Leu Thr Ala Ala  
225 230 235 240

Pro Val Asn Leu Pro Gly Thr Asn Leu Arg Lys Leu Tyr Leu Gln Asp  
245 250 255

Asn His Ile Asn Arg Val Pro Pro Asn Ala Phe Ser Tyr Leu Arg Gln  
260 265 270

Leu Tyr Arg Leu Asp Met Ser Asn Asn Asn Leu Ser Asn Leu Pro Gln  
275                280                285

Gly Ile Phe Asp Asp Leu Asp Asn Ile Thr Gln Leu Ile Leu Arg Asn  
290                295                300

Asn Pro Trp Tyr Cys Gly Cys Lys Met Lys Trp Val Arg Asp Trp Leu  
305                310                315                320

Gln Ser Leu Pro Val Lys Val Asn Val Arg Gly Leu Met Cys Gln Ala  
325                330                335

Pro Glu Lys Val Arg Gly Met Ala Ile Lys Asp Leu Asn Ala Glu Leu  
340                345                350

Phe Asp Cys Lys Asp Ser Gly Ile Val Ser Thr Ile Gln Ile Thr Thr  
355                360                365

Ala Ile Pro Asn Thr Val Tyr Pro Ala Gln Gly Gln Trp Pro Ala Pro  
370                375                380

Val Thr Lys Gln Pro Asp Ile Lys Asn Pro Lys Leu Thr Lys Asp Gln  
385                390                395                400

Gln Thr Thr Gly Ser Pro Ser Arg Lys Thr Ile Thr Ile Thr Val Lys  
405                410                415

Ser Val Thr Ser Asp Thr Ile His Ile Ser Trp Lys Leu Ala Leu Pro  
420                425                430

Met Thr Ala Leu Arg Leu Ser Trp Leu Lys Leu Gly His Ser Pro Ala  
435                440                445

Phe Gly Ser Ile Thr Glu Thr Ile Val Thr Gly Glu Arg Ser Glu Tyr  
450                455                460

Leu Val Thr Ala Leu Glu Pro Asp Ser Pro Tyr Lys Val Cys Met Val  
465                470                475                480

Pro Met Glu Thr Ser Asn Leu Tyr Leu Phe Asp Glu Thr Pro Val Cys  
485                490                495

Ile Glu Thr Glu Thr Ala Pro Leu Arg Met Tyr Asn Pro Thr Thr Thr  
500                505                510

Leu Asn Arg Glu Gln Glu Lys Glu Pro Tyr Lys Asn Pro Asn Leu Pro  
515                520                525

Leu Ala Ala Ile Ile Gly Gly Ala Val Ala Leu Val Thr Ile Ala Leu  
530                535                540

Leu Ala Leu Val Cys Trp Tyr Val His Arg Asn Gly Ser Leu Phe Ser  
545                550                555                560

Arg Asn Cys Ala Tyr Ser Lys Gly Arg Arg Arg Lys Asp Asp Tyr Ala  
565                570                575

Glu Ala Gly Thr Lys Lys Asp Asn Ser Ile Leu Glu Ile Arg Glu Thr  
580                585                590

Ser Phe Gln Met Leu Pro Ile Ser Asn Glu Pro Ile Ser Lys Glu Glu  
595                600                605

Phe Val Ile His Thr Ile Phe Pro Pro Asn Gly Met Asn Leu Tyr Lys  
610                615                620

Asn Asn His Ser Glu Ser Ser Asn Arg Ser Tyr Arg Asp Ser Gly  
625                630                635                640

Ile Pro Asp Ser Asp His Ser His Ser  
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<210> 7

<211> 1653

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (964)..(1443)

<400> 7

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actttttta ttcttttt tccatctctg ggccagctg ggatcctagg ccgcctggg 120

aagacatttg tgtttacac acataaggat ctgtgtttgg ggtttctct tcctccctg 180

acattggcat tgcttagtg ttgtgtggg agggagacca cgtggctca gtgttgctt 240

gcacttatct gccttaggtac atcgaagtct ttgacacctc atacagtgtat tatgcctgtc 300

atcgctggc gtatcctggc ggcctgctc ctgtgatag ttgtcgtct ctgtcttac 360

tc当地atac acaacgcgtc aaaagctgca aaggaacctg aagctgtggc tgtaaaaaat 420

cacaacccag acaaggtgtg gtggccaag aacagccagg ccaaaccat tgccacggag 480

tcttgtctg ccctgcagtg ctgtgaagga tatagaatgt gtgccagtt tgattccctg 540

ccacccctg ctgtgcacat aaatgagggc ctctgatggaaaggctc cttctcaaa 600

gcagagccct gaagacttca atgatgtcaa tgaggccacc tgtttgtat gtgcaggcac 660

agaagaaaagg cacagctccc catcagtttc atggaaaata actcagtgcc tgctggaaac 720  
cagctgctgg agatccctac agagagcttc cactggggc aaccctcca ggaaggagtt 780  
ggggagagag aaccctact gtggggaatg ctgataaaccc agtcacacag ctgcctatt 840  
ctcacacaaa tctacccctt gcgtggctgg aactgacgtt tccctggagg tgtccagaaa 900  
gctgatgtaa cacagagcct ataaaagctg tcggcccta aggctgccc gcgcctgcc 960  
aaa atg gag ctt gta aga agg ctc atg cca ttg acc ctc tta att ctc 1008  
Met Glu Leu Val Arg Arg Leu Met Pro Leu Thr Leu Leu Ile Leu  
1 5 10 15  
tcc tgt ttg gcg gag ctg aca atg gcg gag gct gaa ggc aat gca agc 1056  
Ser Cys Leu Ala Glu Leu Thr Met Ala Glu Ala Glu Asn Ala Ser  
20 25 30  
tgc aca gtc agt cta ggg ggt gcc aat atg gca gag acc cac aaa gcc 1104  
Cys Thr Val Ser Leu Gly Gly Ala Asn Met Ala Glu Thr His Lys Ala  
35 40 45  
atg atc ctg caa ctc aat ccc agt gag aac tgc acc tgg aca ata gaa 1152  
Met Ile Leu Gln Leu Asn Pro Ser Glu Asn Cys Thr Trp Thr Ile Glu  
50 55 60  
aga cca gaa aac aaa agc atc aga att atc ttt tcc tat gtc cag ctt 1200  
Arg Pro Glu Asn Lys Ser Ile Arg Ile Ile Phe Ser Tyr Val Gln Leu  
65 70 75  
gat cca gat gga agc tgt gaa agt gaa aac att aaa gtc ttt gac gga 1248  
Asp Pro Asp Gly Ser Cys Glu Ser Glu Asn Ile Lys Val Phe Asp Gly  
80 85 90 95  
acc tcc agc aat ggg cct ctg cta ggg caa gtc tgc agt aaa aac gac 1296  
Thr Ser Ser Asn Gly Pro Leu Leu Gly Gln Val Cys Ser Lys Asn Asp  
100 105 110  
tat gtt cct gta ttt gaa tca tca tcc agt aca ttg acg ttt caa ata 1344  
Tyr Val Pro Val Phe Glu Ser Ser Ser Thr Leu Thr Phe Gln Ile  
115 120 125  
gtt act gac tca gca aga att caa aga act gtc ttt gtc ttc tac tac 1392  
Val Thr Asp Ser Ala Arg Ile Gln Arg Thr Val Phe Val Phe Tyr Tyr  
130 135 140  
ttc ttc tct cct aac atc tgg ctc tgc att cac agc acc tac att cca 1440  
Phe Phe Ser Pro Asn Ile Trp Leu Cys Ile His Ser Thr Tyr Ile Pro  
145 150 155  
ctg tgatccgaag cagaatgccca agaacatctg cgagtgggtt catgaggaga 1493  
Leu  
160

gctccactgt ggattcttt ccaaggccca gagctgacca tgcactctc ctgctaaaac 1553  
cactgacttc ttggtaccag cagatctcca gagtgacca gtcagggtt tcccacgctg 1613  
gaccaggccc ctgtcccatc aaaaaaaaaa aaaaaaaaaa 1653

<210> 8  
<211> 160  
<212> PRT  
<213> Homo sapiens

<400> 8  
Met Glu Leu Val Arg Arg Leu Met Pro Leu Thr Leu Leu Ile Leu Ser  
1 5 10 15

Cys Leu Ala Glu Leu Thr Met Ala Glu Ala Glu Gly Asn Ala Ser Cys  
20 25 30

Thr Val Ser Leu Gly Gly Ala Asn Met Ala Glu Thr His Lys Ala Met  
35 40 45

Ile Leu Gln Leu Asn Pro Ser Glu Asn Cys Thr Trp Thr Ile Glu Arg  
50 55 60

Pro Glu Asn Lys Ser Ile Arg Ile Ile Phe Ser Tyr Val Gln Leu Asp  
65 70 75 80

Pro Asp Gly Ser Cys Glu Ser Glu Asn Ile Lys Val Phe Asp Gly Thr  
85 90 95

Ser Ser Asn Gly Pro Leu Leu Gly Gln Val Cys Ser Lys Asn Asp Tyr  
100 105 110

Val Pro Val Phe Glu Ser Ser Ser Thr Leu Thr Phe Gln Ile Val  
115 120 125

Thr Asp Ser Ala Arg Ile Gln Arg Thr Val Phe Val Phe Tyr Tyr Phe  
130 135 140

Phe Ser Pro Asn Ile Trp Leu Cys Ile His Ser Thr Tyr Ile Pro Leu  
145 150 155 160

<210> 9  
<211> 2478  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS

<222> (273)..(2012)

<400> 9

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agggtgcctc tcttgagaag aactgtccat accatggtgg tggtaaggct ttaccagg 180  
ctcaggatgc ccataggat gggtaagcc tgccctggctt gtgggtctt ccagtggccg 240  
tcatctcatt agggccccac agtggcatta gg atg cac ctc tcg gcg gtg ttc 293  
Met His Leu Ser Ala Val Phe  
1 5

aac gcc ctc ctg gtg tcg ctg gca gcg gtc ctg tgg aag cat gtg 341  
Asn Ala Leu Leu Val Ser Val Leu Ala Ala Val Leu Trp Lys His Val  
10 15 20

cgg ctg cgt gag cat gca gcc aca ctg gag gag ctg gcc ctc agc 389  
Arg Leu Arg Glu His Ala Ala Thr Leu Glu Glu Leu Ala Leu Ser  
25 30 35

cga cag gcc aca gag cca gca ctg agg atc gac tac ccg aag 437  
Arg Gln Ala Thr Glu Pro Ala Pro Ala Leu Arg Ile Asp Tyr Pro Lys  
40 45 50 55

gca ctg cag atc ctg atg gag ggc ggc aca cac atg gtg tgc acg ggc 485  
Ala Leu Gln Ile Leu Met Glu Gly Gly Thr His Met Val Cys Thr Gly  
60 65 70

cgc acg cac aca gac cgc atc tgc cgc ttc aag tgg ctc tgc tac tcc 533  
Arg Thr His Thr Asp Arg Ile Cys Arg Phe Lys Trp Leu Cys Tyr Ser  
75 80 85

aac gag gct gag gag ttc atc ttc ttc cat ggc aac acc tct gtc atg 581  
Asn Glu Ala Glu Glu Phe Ile Phe Phe His Gly Asn Thr Ser Val Met  
90 95 100

ctg ccc aac ctg ggc tcc cgg cgc ttc cag cca gcc ctg ctc gac cta 629  
Leu Pro Asn Leu Gly Ser Arg Arg Phe Gln Pro Ala Leu Leu Asp Leu  
105 110 115

tcc acc gtg gag gac cac aac act cag tac ttc aac ttc gtg gag ctg 677  
Ser Thr Val Glu Asp His Asn Thr Gln Tyr Phe Asn Phe Val Glu Leu  
120 125 130 135

cct gct gct gcc ctg cgc ttc atg ccc aag ccg gtg ttc gtg cca gac 725  
Pro Ala Ala Ala Leu Arg Phe Met Pro Lys Pro Val Phe Val Pro Asp  
140 145 150

gtg gcc ctc atc gcc aac cgc ttc aac ccc gac aac ctc atg cac gtc 773  
Val Ala Leu Ile Ala Asn Arg Phe Asn Pro Asp Asn Leu Met His Val

155

160

165

ttt cat gac gac ctg ctg cca ctc ttc tac acc ctg cgg cag ttt ccc 821  
Phe His Asp Asp Leu Leu Pro Leu Phe Tyr Thr Leu Arg Gln Phe Pro  
170 175 180

ggc ctg gcc cac gag gca cgg ctc ttc atg gag ggc tgg ggc gag 869  
Gly Leu Ala His Glu Ala Arg Leu Phe Phe Met Glu Gly Trp Gly Glu  
185 190 195

ggt gca cac ttc gac ctc tac aag ctg ctc agc ccc aag cag cct ctc 917  
Gly Ala His Phe Asp Leu Tyr Lys Leu Leu Ser Pro Lys Gln Pro Leu  
200 205 210 215

ctg cgg gca cag ctg aag acc ctg ggc cgg ctg ctg tgc ttc tcc cat 965  
Leu Arg Ala Gln Leu Lys Thr Leu Gly Arg Leu Leu Cys Phe Ser His  
220 225 230

gct ttt gtg ggc ctc tcc aag atc act acc tgg tac cag tat ggc ttt 1013  
Ala Phe Val Gly Leu Ser Lys Ile Thr Thr Trp Tyr Gln Tyr Gly Phe  
235 240 245

gtg cag ccc cag ggc ccg aag gcc aac atc ctc gtc tca ggc aat gag 1061  
Val Gln Pro Gln Gly Pro Lys Ala Asn Ile Leu Val Ser Gly Asn Glu  
250 255 260

atc cgg cag ttt gca cgg ttc atg aca gaa aag ctg aac gtg agc cac 1109  
Ile Arg Gln Phe Ala Arg Phe Met Thr Glu Lys Leu Asn Val Ser His  
265 270 275

aca gga gtc ccc cta ggc gag gag tac att ctg gtc ttt agc cga acc 1157  
Thr Gly Val Pro Leu Gly Glu Tyr Ile Leu Val Phe Ser Arg Thr  
280 285 290 295

cag aac aga ctc att ctg aat gag gca gag ctg ctg ctg gca ctg gcc 1205  
Gln Asn Arg Leu Ile Leu Asn Glu Ala Glu Leu Leu Ala Leu Ala  
300 305 310

cag gag ttc cag atg aag aca gtg aca gtg tcc ctg gag gac cac acc 1253  
Gln Glu Phe Gln Met Lys Thr Val Thr Val Ser Leu Glu Asp His Thr  
315 320 325

ttt gct gat gtc gtg cgg ctg gtc agc aat gcc tcc atg ctg gtc agc 1301  
Phe Ala Asp Val Val Arg Leu Val Ser Asn Ala Ser Met Leu Val Ser  
330 335 340

atg cat ggg gcc cag ctg gtc acc acc ctc ttc ctg ccc cgt ggg gca 1349  
Met His Gly Ala Gln Leu Val Thr Thr Leu Phe Leu Pro Arg Gly Ala  
345 350 355

act gtg gta gag ctc ttc cca tat gct aat ccc gac cac tac act 1397  
Thr Val Val Glu Leu Phe Pro Tyr Ala Val Asn Pro Asp His Tyr Thr  
360 365 370 375

ccc tat aag acg ctg gcc atg ctg cct ggc atg gac ctc cag tat gta 1445  
Pro Tyr Lys Thr Leu Ala Met Leu Pro Gly Met Asp Leu Gln Tyr Val  
380 385 390

gcc tgg cggtt aac atg atg cca gag aac aca gtc aca cac cct gag cggtt 1493  
Ala Trp Arg Asn Met Met Pro Glu Asn Thr Val Thr His Pro Glu Arg  
395 400 405

ccc tgg gat cag ggg ggc atc acc cat ctg gac cggtt gag caa gcc 1541  
Pro Trp Asp Gln Gly Gly Ile Thr His Leu Asp Arg Ala Glu Gln Ala  
410 415 420

cgt atc ctg caa agc cgt gag gtc cca cggtt cat ctc tgt tgc cggtt aac 1589  
Arg Ile Leu Gln Ser Arg Glu Val Pro Arg His Leu Cys Cys Arg Asn  
425 430 435

ccc gag tgg ctc ttc cga atc tac cag gac acc aag gtg gac atc cca 1637  
Pro Glu Trp Leu Phe Arg Ile Tyr Gln Asp Thr Lys Val Asp Ile Pro  
440 445 450 455

tcc ctc att caa acc ata cggtt cgc gtg gtg aag ggc cggtt cca gga cca 1685  
Ser Leu Ile Gln Thr Ile Arg Arg Val Val Lys Gly Arg Pro Gly Pro  
460 465 470

cggtt aag cag aag tgg aca gtc ggc cta tat cca gggtt aag gtg cggtt gag 1733  
Arg Lys Gln Lys Trp Thr Val Gly Leu Tyr Pro Gly Lys Val Arg Glu  
475 480 485

gca cggtt tgc cag ggc tca gtg cat ggc gtc tcc gag gtc cggtt ctc act 1781  
Ala Arg Cys Gln Ala Ser Val His Gly Ala Ser Glu Ala Arg Leu Thr  
490 495 500

gtc tcc tgg cag atc cca tgg aac ctt aaa tac ctg aag gtg agg gag 1829  
Val Ser Trp Gln Ile Pro Trp Asn Leu Lys Tyr Leu Lys Val Arg Glu  
505 510 515

gtg aag tac gag gtg tgg ctg cag gag cag ggg gag aac acc tac gtg 1877  
Val Lys Tyr Glu Val Trp Leu Gln Glu Gln Gly Glu Asn Thr Tyr Val  
520 525 530 535

cct tac atc ctg gct ctg cag aac cac acc ttc act gag aac atc aag 1925  
Pro Tyr Ile Leu Ala Leu Gln Asn His Thr Phe Thr Glu Asn Ile Lys  
540 545 550

ccc ttc acc acc tac ctg gtg tgg gtc cggtt tgc atc ttc aac aag atc 1973  
Pro Phe Thr Thr Tyr Leu Val Trp Val Arg Cys Ile Phe Asn Lys Ile  
555 560 565

ctc ctg gga ccc ttt gca gat gtg ctg gtg tgc aac acg tagcgagcag 2022  
Leu Leu Gly Pro Phe Ala Asp Val Leu Val Cys Asn Thr  
570 575 580

gccacagcct ggcctcgga aggtggctcc tgcaagttag cgtccctggg cccattaatc 2082  
ccactgtgga gacttctggg aactatttat tgagcaggcc tgcgcctcca catcatctg 2142  
ttgtctctgg ggtgtgggtcacagcactc ctcttgccc tagagataag ggacctgact 2202  
tcccctctc ccattcctgaa catttgtacc cctggagaag ttcccttagca gggaggagga 2262  
agaggagagg aggaagcaa gaatcacaag gaacctctgg cttaggtgatc ctgtatgttc 2322  
ctactgagtt ttctggat ccagattct ggaaaccgcg taatcatgtatctgtt 2382  
gggtggttca tctgcctcca tcccagtgaa atttacctgt agcccaagtga agggtggtt 2442  
tggaacattc attaaatgt tctaagcgaa aaaaaaa 2478

<210> 10  
<211> 580  
<212> PRT  
<213> Homo sapiens

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Ala Val Leu Trp Lys His Val Arg Leu Arg Glu His Ala Ala Thr Leu  
20 25 30  
  
Glu Glu Glu Leu Ala Leu Ser Arg Gln Ala Thr Glu Pro Ala Pro Ala  
35 40 45  
  
Leu Arg Ile Asp Tyr Pro Lys Ala Leu Gln Ile Leu Met Glu Gly Gly  
50 55 60  
  
Thr His Met Val Cys Thr Gly Arg Thr His Thr Asp Arg Ile Cys Arg  
65 70 75 80  
  
Phe Lys Trp Leu Cys Tyr Ser Asn Glu Ala Glu Glu Phe Ile Phe Phe  
85 90 95  
  
His Gly Asn Thr Ser Val Met Leu Pro Asn Leu Gly Ser Arg Arg Phe  
100 105 110  
  
Gln Pro Ala Leu Leu Asp Leu Ser Thr Val Glu Asp His Asn Thr Gln  
115 120 125  
  
Tyr Phe Asn Phe Val Glu Leu Pro Ala Ala Leu Arg Phe Met Pro  
130 135 140  
  
Lys Pro Val Phe Val Pro Asp Val Ala Leu Ile Ala Asn Arg Phe Asn  
145 150 155 160

Pro Asp Asn Leu Met His Val Phe His Asp Asp Leu Leu Pro Leu Phe  
165 170 175

Tyr Thr Leu Arg Gln Phe Pro Gly Leu Ala His Glu Ala Arg Leu Phe  
180 185 190

Phe Met Glu Gly Trp Gly Glu Ala His Phe Asp Leu Tyr Lys Leu  
195 200 205

Leu Ser Pro Lys Gln Pro Leu Leu Arg Ala Gln Leu Lys Thr Leu Gly  
210 215 220

Arg Leu Leu Cys Phe Ser His Ala Phe Val Gly Leu Ser Lys Ile Thr  
225 230 235 240

Thr Trp Tyr Gln Tyr Gly Phe Val Gln Pro Gln Gly Pro Lys Ala Asn  
245 250 255

Ile Leu Val Ser Gly Asn Glu Ile Arg Gln Phe Ala Arg Phe Met Thr  
260 265 270

Glu Lys Leu Asn Val Ser His Thr Gly Val Pro Leu Gly Glu Tyr  
275 280 285

Ile Leu Val Phe Ser Arg Thr Gln Asn Arg Leu Ile Leu Asn Glu Ala  
290 295 300

Glu Leu Leu Ala Leu Ala Gln Glu Phe Gln Met Lys Thr Val Thr  
305 310 315 320

Val Ser Leu Glu Asp His Thr Phe Ala Asp Val Val Arg Leu Val Ser  
325 330 335

Asn Ala Ser Met Leu Val Ser Met His Gly Ala Gln Leu Val Thr Thr  
340 345 350

Leu Phe Leu Pro Arg Gly Ala Thr Val Val Glu Leu Phe Pro Tyr Ala  
355 360 365

Val Asn Pro Asp His Tyr Thr Pro Tyr Lys Thr Leu Ala Met Leu Pro  
370 375 380

Gly Met Asp Leu Gln Tyr Val Ala Trp Arg Asn Met Met Pro Glu Asn  
385 390 395 400

Thr Val Thr His Pro Glu Arg Pro Trp Asp Gln Gly Gly Ile Thr His  
405 410 415

Leu Asp Arg Ala Glu Gln Ala Arg Ile Leu Gln Ser Arg Glu Val Pro  
420 425 430

Arg His Leu Cys Cys Arg Asn Pro Glu Trp Leu Phe Arg Ile Tyr Gln  
435 440 445

Asp Thr Lys Val Asp Ile Pro Ser Leu Ile Gln Thr Ile Arg Arg Val  
450                  455                  460

Val Lys Gly Arg Pro Gly Pro Arg Lys Gln Lys Trp Thr Val Gly Leu  
465                  470                  475                  480

Tyr Pro Gly Lys Val Arg Glu Ala Arg Cys Gln Ala Ser Val His Gly  
485                  490                  495

Ala Ser Glu Ala Arg Leu Thr Val Ser Trp Gln Ile Pro Trp Asn Leu  
500                  505                  510

Lys Tyr Leu Lys Val Arg Glu Val Lys Tyr Glu Val Trp Leu Gln Glu  
515                  520                  525

Gln Gly Glu Asn Thr Tyr Val Pro Tyr Ile Leu Ala Leu Gln Asn His  
530                  535                  540

Thr Phe Thr Glu Asn Ile Lys Pro Phe Thr Thr Tyr Leu Val Trp Val  
545                  550                  555                  560

Arg Cys Ile Phe Asn Lys Ile Leu Leu Gly Pro Phe Ala Asp Val Leu  
565                  570                  575

Val Cys Asn Thr  
580

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<220>  
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<222> (141)..(503)

<400> 11  
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tttacgaccc acagatttag gcccgtattc tcttctttt caggaatgtg cacctcaccc 120

tgttctccca gacctgggg atg aag gaa aca gga gcc tca ccc agg agg ctc 173  
Met Lys Glu Thr Gly Ala Ser Pro Arg Arg Leu  
1                  5                  10

aag gcc aaa act ctg acc caa act acc tca gga gcc cct ggc cct ggc 221  
Lys Ala Lys Thr Leu Thr Gln Thr Thr Ser Gly Ala Pro Gly Pro Gly  
15                  20                  25

ttc ccc cct gct cca gag ttt ctg ccc tgc cca cac aca cac acc ctc 269

Phe Pro Pro Ala Pro Glu Phe Leu Pro Cys Pro His Thr His Thr Leu  
30 35 40

ttc cac cct cag agg ccc cgg tgt cct gcc cca cgc tct acc cca gag 317  
Phe His Pro Gln Arg Pro Arg Cys Pro Ala Pro Arg Ser Thr Pro Glu  
45 50 55

ccc cac ggg tgg ctt tat aaa agt gcc ggg ccc agc cct cta gca gga 365  
Pro His Gly Trp Leu Tyr Lys Ser Ala Gly Pro Ser Pro Leu Ala Gly  
60 65 70 75

ggg gaa tgc tgg gca tct ggg tgt ggg acc ccc ggg gaa cag cct gtg 413  
Gly Glu Cys Trp Ala Ser Gly Cys Gly Thr Pro Gly Glu Gln Pro Val  
80 85 90

gtc tgg act cct gca tct atg agg gga cag acg tgg ctt ccc ttc cgg 461  
Val Trp Thr Pro Ala Ser Met Arg Gly Gln Thr Trp Leu Pro Phe Arg  
95 100 105

atg atg ggg tac cca cag atg gag gcc agg gtc cct caa 503  
Met Met Gly Tyr Pro Gln Met Met Glu Ala Arg Val Pro Gln  
110 115 120

taaaagaagg ggtgcaaaaa 523

<210> 12  
<211> 121  
<212> PRT  
<213> Homo sapiens

<400> 12  
Met Lys Glu Thr Gly Ala Ser Pro Arg Arg Leu Lys Ala Lys Thr Leu  
1 5 10 15

Thr Gln Thr Thr Ser Gly Ala Pro Gly Pro Gly Phe Pro Pro Ala Pro  
20 25 30

Glu Phe Leu Pro Cys Pro His Thr His Thr Leu Phe His Pro Gln Arg  
35 40 45

Pro Arg Cys Pro Ala Pro Arg Ser Thr Pro Glu Pro His Gly Trp Leu  
50 55 60

Tyr Lys Ser Ala Gly Pro Ser Pro Leu Ala Gly Gly Glu Cys Trp Ala  
65 70 75 80

Ser Gly Cys Gly Thr Pro Gly Glu Gln Pro Val Val Trp Thr Pro Ala  
85 90 95

Ser Met Arg Gly Gln Thr Trp Leu Pro Phe Arg Met Met Gly Tyr Pro  
100 105 110

Gln Met Met Glu Ala Arg Val Pro Gln  
115 120

<210> 13  
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<220>  
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<222> (178)..(3156)

<220>  
<223> n 1755 can be A, G, C, or T

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ctgcggcccc gctccctcta cccggccgga cccggctctg ccccccgcgc caagccccac 120  
caagcccccc gccctcccgcc cgccggtccca gcccaggggcg cggccgcaac cagcacc 177  
atg cgc ccg gta gcc ctg ctg ctc ctg ccc tcg ctg ctg gcg ctc ctg 225  
Met Arg Pro Val Ala Leu Leu Leu Leu Pro Ser Leu Leu Ala Leu Leu  
1 5 10 15

gct cac gga ctc tct tta gag gcc cca acc gtg ggg aaa gga caa gcc 273  
Ala His Gly Leu Ser Leu Glu Ala Pro Thr Val Gly Lys Gly Gln Ala  
20 25 30

cca ggc atc gag gag aca gat ggc gag ctg aca gca gcc ccc aca cct 321  
Pro Gly Ile Glu Glu Thr Asp Gly Glu Leu Thr Ala Ala Pro Thr Pro  
35 40 45

gag cag cca gaa cga ggc gtc cac ttt gtc aca aca gcc ccc acc ttg 369  
Glu Gln Pro Glu Arg Gly Val His Phe Val Thr Thr Ala Pro Thr Leu  
50 55 60

aag ctg ctc aac cac cac ccg ctg ctt gag gaa ttc cta caa gag ggg 417  
Lys Leu Leu Asn His His Pro Leu Leu Glu Phe Leu Gln Glu Gly  
65 70 75 80

ctg gaa aag gga gat gag gag ctg agg cca gca ctg ccc ttc cag cct 465  
Leu Glu Lys Gly Asp Glu Glu Arg Pro Ala Leu Pro Phe Gln Pro  
85 90 95

gac cca cct gca ccc ttc acc cca agt ccc ctt ccc cgc ctg gcc aac 513  
Asp Pro Pro Ala Pro Phe Thr Pro Ser Pro Leu Pro Arg Leu Ala Asn  
100 105 110

cag gac agc cgc cct gtc ttt acc agc ccc act cca gcc atg gct gcg 561

Gln Asp Ser Arg Pro Val Phe Thr Ser Pro Thr Pro Ala Met Ala Ala  
115 120 125

gta ccc act cag ccc cag tcc aag gag gga ccc tgg agt ccg gag tca 609  
Val Pro Thr Gln Pro Gln Ser Lys Glu Gly Pro Trp Ser Pro Glu Ser  
130 135 140

gag tcc cct atg ctt cga atc aca gct ccc cta cct cca ggg ccc agc 657  
Glu Ser Pro Met Leu Arg Ile Thr Ala Pro Leu Pro Pro Gly Pro Ser  
145 150 155 160

atg gca gtg ccc acc cta ggc cca ggg gag ata gcc agc act aca ccc 705  
Met Ala Val Pro Thr Leu Gly Pro Gly Glu Ile Ala Ser Thr Thr Pro  
165 170 175

ccc agc aga gcc tgg aca cca acc caa gag ggt cct gga gac atg gga 753  
Pro Ser Arg Ala Trp Thr Pro Thr Gln Glu Gly Pro Gly Asp Met Gly  
180 185 190

agg ccg tgg gtt gca gag gtt gtg tcc cag ggc gca ggg atc ggg atc 801  
Arg Pro Trp Val Ala Glu Val Val Ser Gln Gly Ala Gly Ile Gly Ile  
195 200 205

cag ggg acc atc acc tcc tcc aca gct tca gga gat gat gag gag acc 849  
Gln Gly Thr Ile Thr Ser Ser Thr Ala Ser Gly Asp Asp Glu Glu Thr  
210 215 220

acc act acc acc acc atc atc acc acc atc acc aca gtc cag aca 897  
Thr Thr Thr Thr Ile Ile Thr Thr Ile Thr Thr Val Gln Thr  
225 230 235 240

cca ggc cct tgt agc tgg aat ttc tca ggc cca gag ggc tct ctg gac 945  
Pro Gly Pro Cys Ser Trp Asn Phe Ser Gly Pro Glu Gly Ser Leu Asp  
245 250 255

tcc cct aca gac ctc agc tcc ccc act gat gtt ggc ctg gac tgc ttc 993  
Ser Pro Thr Asp Leu Ser Ser Pro Thr Asp Val Gly Leu Asp Cys Phe  
260 265 270

ttc tac atc tct gtc tac cct ggc tat ggc gtg gaa atc aag gtc cag 1041  
Phe Tyr Ile Ser Val Tyr Pro Gly Tyr Gly Val Glu Ile Lys Val Gln  
275 280 285

aat atc agc ctc cgg gaa ggg gag aca gtg act gtg gaa ggc ctg ggg 1089  
Asn Ile Ser Leu Arg Glu Gly Glu Thr Val Thr Val Glu Gly Leu Gly  
290 295 300

ggg cct gac cca ctg ccc ctg gcc aac cag tct ttc ctg ctg cgg ggc 1137  
Gly Pro Asp Pro Leu Pro Leu Ala Asn Gln Ser Phe Leu Leu Arg Gly  
305 310 315 320

caa gtc atc cgc agc ccc acc cac caa gcg gcc ctg agg ttc cag agc 1185  
Gln Val Ile Arg Ser Pro Thr His Gln Ala Ala Leu Arg Phe Gln Ser

325                  330                  335

ctc ccg cca ccg gct ggc cct ggc acc ttc cat ttc cat tac caa gcc 1233  
Leu Pro Pro Pro Ala Gly Pro Gly Thr Phe His Phe His Tyr Gln Ala  
340                  345                  350

tat ctc ctg agc tgc cac ttt ccc cgt cgt caa gct tat gaa gat gtg 1281  
Tyr Leu Leu Ser Cys His Phe Pro Arg Arg Gln Ala Tyr Glu Asp Val  
355                  360                  365

act gtc acc agc atc cac cca gga ggt agt gcc cgc ttc cat tgt gca 1329  
Thr Val Thr Ser Ile His Pro Gly Gly Ser Ala Arg Phe His Cys Ala  
370                  375                  380

act ggc tac cag ctg aag ggc agg cat ctc acc tgt ctc aat gcc 1377  
Thr Gly Tyr Gln Leu Lys Gly Ala Arg His Leu Thr Cys Leu Asn Ala  
385                  390                  395                  400

acc cag ccc atc tgg gat tca aag gag ccc gta tgc atc gct gct tgc 1425  
Thr Gln Pro Ile Trp Asp Ser Lys Glu Pro Val Cys Ile Ala Ala Cys  
405                  410                  415

ggc gga gtg atc cgc aat gcc acc acc ggc cgc atc gtc tct cca ggc 1473  
Gly Gly Val Ile Arg Asn Ala Thr Thr Gly Arg Ile Val Ser Pro Gly  
420                  425                  430

ttc ccg ggc aac tac agc aac aac ctc acc tgt cac tgg ctg ctt gag 1521  
Phe Pro Gly Asn Tyr Ser Asn Asn Leu Thr Cys His Trp Leu Leu Glu  
435                  440                  445

gct cct gag ggc cag cgg cta cac ctg cac ttt gag aag gtt tcc ctg 1569  
Ala Pro Glu Gly Gln Arg Leu His Leu His Phe Glu Lys Val Ser Leu  
450                  455                  460

gca gag gat gat gac agg ctc atc att cgc aat ggg gac aac gtg gag 1617  
Ala Glu Asp Asp Asp Arg Leu Ile Ile Arg Asn Gly Asp Asn Val Glu  
465                  470                  475                  480

gcc cca cca gtg tat gat tcc tat gag gtg gaa tac ctg ccc att gag 1665  
Ala Pro Pro Val Tyr Asp Ser Tyr Glu Val Glu Tyr Leu Pro Ile Glu  
485                  490                  495

ggc ctg ctc agc tct ggc aaa cac ttc ttt gtt gag ctc agt act gac 1713  
Gly Leu Leu Ser Ser Gly Lys His Phe Phe Val Glu Leu Ser Thr Asp  
500                  505                  510

agc agc ggg gca gct gca ggc atg gcc ctg cgc tat gag gcn ttc cag 1761  
Ser Ser Gly Ala Ala Ala Gly Met Ala Leu Arg Tyr Glu Ala Phe Gln  
515                  520                  525

cag ggc cat tgc tat gag ccc ttt gtc aaa tac ggt aac ttc agc agc 1809  
Gln Gly His Cys Tyr Glu Pro Phe Val Lys Tyr Gly Asn Phe Ser Ser  
530                  535                  540

agc aca ccc acc tac cct gtg ggt acc act gtg gag ttt agc tgc gac 1857  
Ser Thr Pro Thr Tyr Pro Val Gly Thr Thr Val Glu Phe Ser Cys Asp  
545 550 555 560

cct ggc tac acc ctg gag cag ggc tcc atc atc gag tgt gtt gac 1905  
Pro Gly Tyr Thr Leu Glu Gln Gly Ser Ile Ile Ile Glu Cys Val Asp  
565 570 575

ccc cac gac ccc cag tgg aat gag aca gag cca gcc tgc cga gcc gtg 1953  
Pro His Asp Pro Gln Trp Asn Glu Thr Glu Pro Ala Cys Arg Ala Val  
580 585 590

tgc agc ggg gag atc aca gac tgg gtc gta ctc tct ccc aac 2001  
Cys Ser Gly Glu Ile Thr Asp Ser Ala Gly Val Val Leu Ser Pro Asn  
595 600 605

tgg cca gag ccc tac agt cgt ggg cag gat tgt atc tgg ggt gtg cat 2049  
Trp Pro Glu Pro Tyr Ser Arg Gly Gln Asp Cys Ile Trp Gly Val His  
610 615 620

gtg gaa gag gac aag cgc atc atg ctg gac atc cga gtg ctg cgc ata 2097  
Val Glu Glu Asp Lys Arg Ile Met Leu Asp Ile Arg Val Leu Arg Ile  
625 630 635 640

ggc cct ggt gat gtg ctt acc ttc tat gat ggg gat gac ctg acg gcc 2145  
Gly Pro Gly Asp Val Leu Thr Phe Tyr Asp Gly Asp Asp Leu Thr Ala  
645 650 655

cgg gtt ctg ggc cag tac tca ggg ccc cgt agc cac ttc aag ctc ttt 2193  
Arg Val Leu Gly Gln Tyr Ser Gly Pro Arg Ser His Phe Lys Leu Phe  
660 665 670

acc tcc atg gct gat gtc acc att cag ttc cag tgc gac ccc ggg acc 2241  
Thr Ser Met Ala Asp Val Thr Ile Gln Phe Gln Ser Asp Pro Gly Thr  
675 680 685

tca gtg ctg ggc tac cag cag ggc ttc gtc atc cac ttc ttt gag gtg 2289  
Ser Val Leu Gly Tyr Gln Gln Gly Phe Val Ile His Phe Phe Glu Val  
690 695 700

ccc cgc aat gac aca tgt ccg gag ctg cct gag atc ccc aat ggc tgg 2337  
Pro Arg Asn Asp Thr Cys Pro Glu Leu Pro Glu Ile Pro Asn Gly Trp  
705 710 715 720

aag agc cca tcg cag cct gag cta gtg cac ggc acc gtg gtc act tac 2385  
Lys Ser Pro Ser Gln Pro Glu Leu Val His Gly Thr Val Val Thr Tyr  
725 730 735

cag tgc tac cct ggc tac cag gta gtg gga tcc agt gtc ctc atg tgc 2433  
Gln Cys Tyr Pro Gly Tyr Gln Val Val Gly Ser Ser Val Leu Met Cys  
740 745 750

cag tgg gac cta act tgg agt gag gac ctg ccc tca tgc cag agg gtg 2481  
Gln Trp Asp Leu Thr Trp Ser Glu Asp Leu Pro Ser Cys Gln Arg Val  
755 760 765

act tcc tgc cac gat cct gga gat gtg gag cac agc cga cgc ctc ata 2529  
Thr Ser Cys His Asp Pro Gly Asp Val Glu His Ser Arg Arg Leu Ile  
770 775 780

tcc agc ccc aag ttt ccc gtg ggg gcc acc gtg caa tat atc tgt gac 2577  
Ser Ser Pro Lys Phe Pro Val Gly Ala Thr Val Gln Tyr Ile Cys Asp  
785 790 795 800

cag ggt ttt gtg ctg acg ggc agc tcc atc ctc acc tgc cat gat cgc 2625  
Gln Gly Phe Val Leu Thr Gly Ser Ser Ile Leu Thr Cys His Asp Arg  
805 810 815

cag gct ggc agc ccc aag tgg agt gac cgg gcc cct aaa tgt ctc ctg 2673  
Gln Ala Gly Ser Pro Lys Trp Ser Asp Arg Ala Pro Lys Cys Leu Leu  
820 825 830

gaa cag ctc aag cca tgc cat ggt ctc agt gcc cct gag aat ggt gcc 2721  
Glu Gln Leu Lys Pro Cys His Gly Leu Ser Ala Pro Glu Asn Gly Ala  
835 840 845

cga agt cct gag aag cag cta cac cca gca ggg gcc acc atc cac ttc 2769  
Arg Ser Pro Glu Lys Gln Leu His Pro Ala Gly Ala Thr Ile His Phe  
850 855 860

tcg tgt gcc cct ggc tat gtg ctg aag ggc cag gcc agc atc aag tgt 2817  
Ser Cys Ala Pro Gly Tyr Val Leu Lys Gly Gln Ala Ser Ile Lys Cys  
865 870 875 880

gtg cct ggg cac ccc tcg cat tgg agt gac ccc cca ccc atc tgt agg 2865  
Val Pro Gly His Pro Ser His Trp Ser Asp Pro Pro Ile Cys Arg  
885 890 895

gct gcc tct ctg gat ggg ttc tac aac agt cgc agc ctg gat gtt gcc 2913  
Ala Ala Ser Leu Asp Gly Phe Tyr Asn Ser Arg Ser Leu Asp Val Ala  
900 905 910

aag gca cct gct gcc tcc agc acc ctg gat gct gcc cac att gca gct 2961  
Lys Ala Pro Ala Ala Ser Ser Thr Leu Asp Ala Ala His Ile Ala Ala  
915 920 925

gcc atc ttc ttg cca ctg gtg gcg atg gtg ttg gta gga ggt gta 3009  
Ala Ile Phe Leu Pro Leu Val Ala Met Val Leu Leu Val Gly Gly Val  
930 935 940

tac ttc tac ttc tcc agg ctc cag gga aaa agc tcc ctg cag ctg ccc 3057  
Tyr Phe Tyr Phe Ser Arg Leu Gln Gly Lys Ser Ser Leu Gln Leu Pro  
945 950 955 960

cgc ccc cgc ccc cgc ccc tac aac cgc att acc ata gag tca gcg ttt 3105

Arg Pro Arg Pro Arg Pro Tyr Asn Arg Ile Thr Ile Glu Ser Ala Phe  
965                    970                    975

gac aat cca act tac gag act gga gag acg aga gaa tat gaa gtc tcc 3153  
Asp Asn Pro Thr Tyr Glu Thr Gly Glu Thr Arg Glu Tyr Glu Val Ser  
980                    985                    990

atc taggtggggg cagtctaggg aagtcaactc agacttgac cacagtccag        3206  
Ile

cagcaaggct ccttgcttcc tgctgtccct ccacccctcg tatataccac ctaggaggag 3266

atgccaccaa gccctaaga agttgtcccc ttccccgcct gcgtatgccta ccatggccta 3326

tttcttgggt gtcattgtccc acttggggcc ctccattggg cccatgtcag ggggcattcta 3386

cctgtggaa gaacatagct ggagcacaag catcaacagc cagcatcctg agccctctca 3446

tgcctggac cagcctggaa cacactagca gagcaggagt acccttcctcc acatgaccac 3506

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cagggtaatc ctcacagcgc catcaccaat ggccaaaact cctctcaacg gtgacctctg 3626

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acagttctgc ctccctgcct gtcccagtgg aggcaaat tctaggagat cctaagggt 3746

tcagggggac cctaccccca cctcaggttg ggctccctg ggcactcatg ctccacacca 3806

aagcaggaca cgccatttc cactgaccac cctataccct gaggaaaggg agacttt 3863

<210> 14

<211> 993

<212> PRT

<213> Homo sapiens

<223> n 1755 can be A, G, C, or T

<400> 14

Met Arg Pro Val Ala Leu Leu Leu Pro Ser Leu Leu Ala Leu Leu

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Ala His Gly Leu Ser Leu Glu Ala Pro Thr Val Gly Lys Gly Gln Ala  
20                    25                    30

Pro Gly Ile Glu Glu Thr Asp Gly Glu Leu Thr Ala Ala Pro Thr Pro  
35                    40                    45

Glu Gln Pro Glu Arg Gly Val His Phe Val Thr Thr Ala Pro Thr Leu  
50                    55                    60

Lys Leu Leu Asn His His Pro Leu Leu Glu Phe Leu Gln Glu Gly

65            70            75            80  
Leu Glu Lys Gly Asp Glu Glu Leu Arg Pro Ala Leu Pro Phe Gln Pro  
85            90            95  
Asp Pro Pro Ala Pro Phe Thr Pro Ser Pro Leu Pro Arg Leu Ala Asn  
100           105           110  
Gln Asp Ser Arg Pro Val Phe Thr Ser Pro Thr Pro Ala Met Ala Ala  
115           120           125  
Val Pro Thr Gln Pro Gln Ser Lys Glu Gly Pro Trp Ser Pro Glu Ser  
130           135           140  
Glu Ser Pro Met Leu Arg Ile Thr Ala Pro Leu Pro Pro Gly Pro Ser  
145           150           155           160  
Met Ala Val Pro Thr Leu Gly Pro Gly Glu Ile Ala Ser Thr Thr Pro  
165           170           175  
Pro Ser Arg Ala Trp Thr Pro Thr Gln Glu Gly Pro Gly Asp Met Gly  
180           185           190  
Arg Pro Trp Val Ala Glu Val Val Ser Gln Gly Ala Gly Ile Gly Ile  
195           200           205  
Gln Gly Thr Ile Thr Ser Ser Thr Ala Ser Gly Asp Asp Glu Glu Thr  
210           215           220  
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225           230           235           240  
Pro Gly Pro Cys Ser Trp Asn Phe Ser Gly Pro Glu Gly Ser Leu Asp  
245           250           255  
Ser Pro Thr Asp Leu Ser Ser Pro Thr Asp Val Gly Leu Asp Cys Phe  
260           265           270  
Phe Tyr Ile Ser Val Tyr Pro Gly Tyr Gly Val Glu Ile Lys Val Gln  
275           280           285  
Asn Ile Ser Leu Arg Glu Gly Glu Thr Val Thr Val Glu Gly Leu Gly  
290           295           300  
Gly Pro Asp Pro Leu Pro Leu Ala Asn Gln Ser Phe Leu Leu Arg Gly  
305           310           315           320  
Gln Val Ile Arg Ser Pro Thr His Gln Ala Ala Leu Arg Phe Gln Ser  
325           330           335  
Leu Pro Pro Ala Gly Pro Gly Thr Phe His Phe His Tyr Gln Ala  
340           345           350

Tyr Leu Leu Ser Cys His Phe Pro Arg Arg Gln Ala Tyr Glu Asp Val  
355            360            365

Thr Val Thr Ser Ile His Pro Gly Gly Ser Ala Arg Phe His Cys Ala  
370            375            380

Thr Gly Tyr Gln Leu Lys Gly Ala Arg His Leu Thr Cys Leu Asn Ala  
385            390            395            400

Thr Gln Pro Ile Trp Asp Ser Lys Glu Pro Val Cys Ile Ala Ala Cys  
405            410            415

Gly Gly Val Ile Arg Asn Ala Thr Thr Gly Arg Ile Val Ser Pro Gly  
420            425            430

Phe Pro Gly Asn Tyr Ser Asn Asn Leu Thr Cys His Trp Leu Leu Glu  
435            440            445

Ala Pro Glu Gly Gln Arg Leu His Leu His Phe Glu Lys Val Ser Leu  
450            455            460

Ala Glu Asp Asp Asp Arg Leu Ile Ile Arg Asn Gly Asp Asn Val Glu  
465            470            475            480

Ala Pro Pro Val Tyr Asp Ser Tyr Glu Val Glu Tyr Leu Pro Ile Glu  
485            490            495

Gly Leu Leu Ser Ser Gly Lys His Phe Phe Val Glu Leu Ser Thr Asp  
500            505            510

Ser Ser Gly Ala Ala Ala Gly Met Ala Leu Arg Tyr Glu Ala Phe Gln  
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Gln Gly His Cys Tyr Glu Pro Phe Val Lys Tyr Gly Asn Phe Ser Ser  
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Ser Thr Pro Thr Tyr Pro Val Gly Thr Thr Val Glu Phe Ser Cys Asp  
545            550            555            560

Pro Gly Tyr Thr Leu Glu Gln Gly Ser Ile Ile Glu Cys Val Asp  
565            570            575

Pro His Asp Pro Gln Trp Asn Glu Thr Glu Pro Ala Cys Arg Ala Val  
580            585            590

Cys Ser Gly Glu Ile Thr Asp Ser Ala Gly Val Val Leu Ser Pro Asn  
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Trp Pro Glu Pro Tyr Ser Arg Gly Gln Asp Cys Ile Trp Gly Val His  
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Val Glu Glu Asp Lys Arg Ile Met Leu Asp Ile Arg Val Leu Arg Ile  
625            630            635            640

Gly Pro Gly Asp Val Leu Thr Phe Tyr Asp Gly Asp Asp Leu Thr Ala  
645 650 655

Arg Val Leu Gly Gln Tyr Ser Gly Pro Arg Ser His Phe Lys Leu Phe  
660 665 670

Thr Ser Met Ala Asp Val Thr Ile Gln Phe Gln Ser Asp Pro Gly Thr  
675 680 685

Ser Val Leu Gly Tyr Gln Gln Gly Phe Val Ile His Phe Phe Glu Val  
690 695 700

Pro Arg Asn Asp Thr Cys Pro Glu Leu Pro Glu Ile Pro Asn Gly Trp  
705 710 715 720

Lys Ser Pro Ser Gln Pro Glu Leu Val His Gly Thr Val Val Thr Tyr  
725 730 735

Gln Cys Tyr Pro Gly Tyr Gln Val Val Gly Ser Ser Val Leu Met Cys  
740 745 750

Gln Trp Asp Leu Thr Trp Ser Glu Asp Leu Pro Ser Cys Gln Arg Val  
755 760 765

Thr Ser Cys His Asp Pro Gly Asp Val Glu His Ser Arg Arg Leu Ile  
770 775 780

Ser Ser Pro Lys Phe Pro Val Gly Ala Thr Val Gln Tyr Ile Cys Asp  
785 790 795 800

Gln Gly Phe Val Leu Thr Gly Ser Ser Ile Leu Thr Cys His Asp Arg  
805 810 815

Gln Ala Gly Ser Pro Lys Trp Ser Asp Arg Ala Pro Lys Cys Leu Leu  
820 825 830

Glu Gln Leu Lys Pro Cys His Gly Leu Ser Ala Pro Glu Asn Gly Ala  
835 840 845

Arg Ser Pro Glu Lys Gln Leu His Pro Ala Gly Ala Thr Ile His Phe  
850 855 860

Ser Cys Ala Pro Gly Tyr Val Leu Lys Gly Gln Ala Ser Ile Lys Cys  
865 870 875 880

Val Pro Gly His Pro Ser His Trp Ser Asp Pro Pro Ile Cys Arg  
885 890 895

Ala Ala Ser Leu Asp Gly Phe Tyr Asn Ser Arg Ser Leu Asp Val Ala  
900 905 910

Lys Ala Pro Ala Ala Ser Ser Thr Leu Asp Ala Ala His Ile Ala Ala

915 920 925

Ala Ile Phe Leu Pro Leu Val Ala Met Val Leu Leu Val Gly Gly Val

930 935 940

Tyr Phe Tyr Phe Ser Arg Leu Gln Gly Lys Ser Ser Leu Gln Leu Pro

945 950 955 960

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Ile

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caagcccccc gccctcccgcc cgccgtccca gcccaggcgcc cggccgcaac cagcaccc 177

atg cgc ccg gta gcc ctg ctg ctc ctg ccc tcg ctg gcg ctc ctg 225

Met Arg Pro Val Ala Leu Leu Leu Pro Ser Leu Leu Ala Leu Leu

1 5 10 15

gct cac gga ctc tct tta gag gcc cca acc gtg ggg aaa gga caa gcc 273

Ala His Gly Leu Ser Leu Glu Ala Pro Thr Val Gly Lys Gly Gln Ala

20 25 30

cca ggc atc gag gag aca gat ggc gag ctg aca gca gcc ccc aca cct 321

Pro Gly Ile Glu Glu Thr Asp Gly Glu Leu Thr Ala Ala Pro Thr Pro

35 40 45

gag cag cca gaa cga ggc gtc cac ttt gtc aca aca gcc ccc acc ttg 369

Glu Gln Pro Glu Arg Gly Val His Phe Val Thr Thr Ala Pro Thr Leu

50 55 60

aag ctg ctc aac cac cac ccg ctg ctt gag gaa ttc cta caa gag ggg 417  
Lys Leu Leu Asn His His Pro Leu Leu Glu Glu Phe Leu Gln Glu Gly  
65 70 75 80

ctg gaa aag gga gat gag gag ctg agg cca gca ctg ccc ttc cag cct 465  
Leu Glu Lys Gly Asp Glu Glu Leu Arg Pro Ala Leu Pro Phe Gln Pro  
85 90 95

gac cca cct gca ccc ttc acc cca agt ccc ctt ccc cgc ctg gcc aac 513  
Asp Pro Pro Ala Pro Phe Thr Pro Ser Pro Leu Pro Arg Leu Ala Asn  
100 105 110

cag gac agc cgc cct gtc ttt acc agc ccc act cca gcc atg gct gcg 561  
Gln Asp Ser Arg Pro Val Phe Thr Ser Pro Thr Pro Ala Met Ala Ala  
115 120 125

gta ccc act cag ccc cag tcc aag gag gga ccc tgg agt ccg gag tca 609  
Val Pro Thr Gln Pro Gln Ser Lys Glu Gly Pro Trp Ser Pro Glu Ser  
130 135 140

gag tcc cct atg ctt cga atc aca gct ccc cta cct cca ggg ccc agc 657  
Glu Ser Pro Met Leu Arg Ile Thr Ala Pro Leu Pro Pro Gly Pro Ser  
145 150 155 160

atg gca gtg ccc acc cta ggc cca ggg gag ata gcc agc act aca ccc 705  
Met Ala Val Pro Thr Leu Gly Pro Gly Glu Ile Ala Ser Thr Thr Pro  
165 170 175

ccc agc aga gcc tgg aca cca acc caa gag ggt cct gga gac atg gga 753  
Pro Ser Arg Ala Trp Thr Pro Thr Gln Glu Gly Pro Gly Asp Met Gly  
180 185 190

agg ccg tgg gtt gca gag gtt gtg tcc cag ggc gca ggg atc ggg atc 801  
Arg Pro Trp Val Ala Glu Val Val Ser Gln Gly Ala Gly Ile Gly Ile  
195 200 205

cag ggg acc atc acc tcc tcc aca gct tca gga gat gat gag gag acc 849  
Gln Gly Thr Ile Thr Ser Ser Thr Ala Ser Gly Asp Asp Glu Glu Thr  
210 215 220

acc act acc acc atc atc acc acc acc atc acc aca gtc cag aca 897  
Thr Thr Thr Thr Ile Ile Thr Thr Thr Ile Thr Thr Val Gln Thr  
225 230 235 240

cca ggc cct tgt agc tgg aat ttc tca ggc cca gag ggc tct ctg gac 945  
Pro Gly Pro Cys Ser Trp Asn Phe Ser Gly Pro Glu Gly Ser Leu Asp  
245 250 255

tcc cct aca gac ctc agc tcc ccc act gat gtt ggc ctg gac tgc ttc 993  
Ser Pro Thr Asp Leu Ser Ser Pro Thr Asp Val Gly Leu Asp Cys Phe  
260 265 270

ttc tac atc tct gtc tac cct ggc tat ggc gtg gaa atc aag gtc cag 1041  
Phe Tyr Ile Ser Val Tyr Pro Gly Tyr Gly Val Glu Ile Lys Val Gln  
275 280 285

aat atc agc ctc cg<sup>g</sup> gaa ggg gag aca gtg act gtg gaa ggc ctg ggg 1089  
Asn Ile Ser Leu Arg Glu Gly Glu Thr Val Thr Val Glu Gly Leu Gly  
290 295 300

ggg cct gac cca ctg ccc ctg gcc aac cag tct ttc ctg ctg cgg ggc 1137  
Gly Pro Asp Pro Leu Pro Ala Asn Gln Ser Phe Leu Leu Arg Gly  
305 310 315 320

caa gtc atc cgc agc ccc acc cac caa gc<sup>g</sup> gcc ctg agg ttc cag agc 1185  
Gln Val Ile Arg Ser Pro Thr His Gln Ala Ala Leu Arg Phe Gln Ser  
325 330 335

ctc ccg cca ccg gct ggc cct ggc acc ttc cat ttc cat tac caa gcc 1233  
Leu Pro Pro Pro Ala Gly Pro Gly Thr Phe His Phe His Tyr Gln Ala  
340 345 350

tat ctc ctg agc tgc cac ttt ccc cgt cgt caa gct tat gaa gat gtg 1281  
Tyr Leu Leu Ser Cys His Phe Pro Arg Arg Gln Ala Tyr Glu Asp Val  
355 360 365

act gtc acc agc atc cac cca gga ggt agt gcc cgc ttc cat tgt gca 1329  
Thr Val Thr Ser Ile His Pro Gly Gly Ser Ala Arg Phe His Cys Ala  
370 375 380

act ggc tac cag ctg aag ggc gcc agg cat ctc acc tgt ctc aat gcc 1377  
Thr Gly Tyr Gln Leu Lys Gly Ala Arg His Leu Thr Cys Leu Asn Ala  
385 390 395 400

acc cag ccc atc tgg gat tca aag gag ccc gta tgc atc gct gct tgc 1425  
Thr Gln Pro Ile Trp Asp Ser Lys Glu Pro Val Cys Ile Ala Ala Cys  
405 410 415

ggc gga gtg atc cgc aat gcc acc acc ggc cgc atc gtc tct cca ggc 1473  
Gly Gly Val Ile Arg Asn Ala Thr Thr Gly Arg Ile Val Ser Pro Gly  
420 425 430

ttc ccg ggc aac tac agc aac aac ctc acc tgt cac tgg ctg ctt gag 1521  
Phe Pro Gly Asn Tyr Ser Asn Asn Leu Thr Cys His Trp Leu Leu Glu  
435 440 445

gct cct gag ggc cag cg<sup>g</sup> cta cac ctg cac ttt gag aag gtt tcc ctg 1569  
Ala Pro Glu Gly Gln Arg Leu His Leu His Phe Glu Lys Val Ser Leu  
450 455 460

gca gag gat gat gac agg ctc atc att cgc aat ggg gac aac gtg gag 1617  
Ala Glu Asp Asp Asp Arg Leu Ile Arg Asn Gly Asp Asn Val Glu  
465 470 475 480

gcc cca cca gtg tat gat tcc tat gag gtg gaa tac ctg ccc att gag 1665

Ala Pro Pro Val Tyr Asp Ser Tyr Glu Val Glu Tyr Leu Pro Ile Glu  
485 490 495

ggc ctg ctc agc tct ggc aaa cac ttc ttt gtt gag ctc agt act gac 1713  
Gly Leu Leu Ser Ser Gly Lys His Phe Phe Val Glu Leu Ser Thr Asp  
500 505 510

agc agc ggg gca gct gca ggc atg gcc ctg cgc tat gag gcn ttc cag 1761  
Ser Ser Gly Ala Ala Ala Gly Met Ala Leu Arg Tyr Glu Ala Phe Gln  
515 520 525

cag ggc cat tgc tat gag ccc ttt gtc aaa tac ggt aac ttc agc agc 1809  
Gln Gly His Cys Tyr Glu Pro Phe Val Lys Tyr Gly Asn Phe Ser Ser  
530 535 540

agc aca ccc acc tac cct gtg ggt acc act gtg gag ttt agc tgc gac 1857  
Ser Thr Pro Thr Tyr Pro Val Gly Thr Val Glu Phe Ser Cys Asp  
545 550 555 560

cct ggc tac acc ctg gag cag ggc tcc atc atc atc gag tgt gtt gac 1905  
Pro Gly Tyr Thr Leu Glu Gln Gly Ser Ile Ile Ile Glu Cys Val Asp  
565 570 575

ccc cac gac ccc cag tgg aat gag aca gag cca gcc tgc cga gcc gtg 1953  
Pro His Asp Pro Gln Trp Asn Glu Thr Glu Pro Ala Cys Arg Ala Val  
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tgc agc ggg gag atc aca gac tcg gct ggc gtg gta ctc tct ccc aac 2001  
Cys Ser Gly Glu Ile Thr Asp Ser Ala Gly Val Val Leu Ser Pro Asn  
595 600 605

tgg cca gag ccc tac agt cgt ggg cag gat tgt atc tgg ggt gtg cat 2049  
Trp Pro Glu Pro Tyr Ser Arg Gly Gln Asp Cys Ile Trp Gly Val His  
610 615 620

gtg gaa gag gac aag cgc atc atg ctg gac atc cga gtg ctg cgc ata 2097  
Val Glu Glu Asp Lys Arg Ile Met Leu Asp Ile Arg Val Leu Arg Ile  
625 630 635 640

ggc cct ggt gat gtg ctt acc ttc tat gat ggg gat gac ctg acg gcc 2145  
Gly Pro Gly Asp Val Leu Thr Phe Tyr Asp Gly Asp Asp Leu Thr Ala  
645 650 655

cgg gtt ctg ggc cag tac tca ggg ccc cgt agc cac ttc aag ctc ttt 2193  
Arg Val Leu Gly Gln Tyr Ser Gly Pro Arg Ser His Phe Lys Leu Phe  
660 665 670

acc tcc atg gct gat gtc acc att cag ttc cag tcg gac ccc ggg acc 2241  
Thr Ser Met Ala Asp Val Thr Ile Gln Phe Gln Ser Asp Pro Gly Thr  
675 680 685

tca gtg ctg ggc tac cag cag ggc ttc gtc atc cac ttc ttt gag gtg 2289  
Ser Val Leu Gly Tyr Gln Gln Gly Phe Val Ile His Phe Phe Glu Val

690            695            700  
ccc cgc aat gac aca tgt ccg gag ctg cct gag atc ccc aat ggc tgg 2337  
Pro Arg Asn Asp Thr Cys Pro Glu Leu Pro Glu Ile Pro Asn Gly Trp  
705            710            715            720  
  
aag agc cca tcg cag cct gag cta gtg cac ggc acc gtg gtc act tac 2385  
Lys Ser Pro Ser Gln Pro Glu Leu Val His Gly Thr Val Val Thr Tyr  
725            730            735  
  
cag tgc tac cct ggc tac cag gta gtg gga tcc agt gtc ctc atg tgc 2433  
Gln Cys Tyr Pro Gly Tyr Gin Val Val Gly Ser Ser Val Leu Met Cys  
740            745            750  
  
cag tgg gac cta act tgg agt gag gac ctg ccc tca tgc cag agg gtg 2481  
Gln Trp Asp Leu Thr Trp Ser Glu Asp Leu Pro Ser Cys Gln Arg Val  
755            760            765  
  
act tcc tgc cac gat cct gga gat gtg gag cac agc cga cgc ctc ata 2529  
Thr Ser Cys His Asp Pro Gly Asp Val Glu His Ser Arg Arg Leu Ile  
770            775            780  
  
tcc agc ccc aag ttt ccc gtg ggg gcc acc gtg caa tat atc tgt gac 2577  
Ser Ser Pro Lys Phe Pro Val Gly Ala Thr Val Gln Tyr Ile Cys Asp  
785            790            795            800  
  
cag ggt ttt gtg ctg acg ggc agc tcc atc ctc acc tgc cat gat cgc 2625  
Gln Gly Phe Val Leu Thr Gly Ser Ser Ile Leu Thr Cys His Asp Arg  
805            810            815  
  
cag gct ggc agc ccc aag tgg agt gac cgg gcc cct aaa tgt ctc ctg 2673  
Gln Ala Gly Ser Pro Lys Trp Ser Asp Arg Ala Pro Lys Cys Leu Leu  
820            825            830  
  
gaa cag ctc aag cca tgc cat ggt ctc agt gcc cct gag aat ggt gcc 2721  
Glu Gln Leu Lys Pro Cys His Gly Leu Ser Ala Pro Glu Asn Gly Ala  
835            840            845  
  
cga agt cct gag aag cag cta cac cca gca ggg gcc acc atc cac ttc 2769  
Arg Ser Pro Glu Lys Gln Leu His Pro Ala Gly Ala Thr Ile His Phe  
850            855            860  
  
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Ser Cys Ala Pro Gly Tyr Val Leu Lys Gly Gln Ala Ser Ile Lys Cys  
865            870            875            880  
  
gtg cct ggg cac ccc tcg cat tgg agt gac ccc cca ccc atc tgt agg 2865  
Val Pro Gly His Pro Ser His Trp Ser Asp Pro Pro Pro Ile Cys Arg  
885            890            895  
  
gct gcc tct ctg gat ggg ttc tac aac agt cgc agc ctg gat gtt gcc 2913  
Ala Ala Ser Leu Asp Gly Phe Tyr Asn Ser Arg Ser Leu Asp Val Ala  
900            905            910

aag gca cct gct gcc tcc agc acc ctg gat gct gcc cac att gca gct 2961  
Lys Ala Pro Ala Ala Ser Ser Thr Leu Asp Ala Ala His Ile Ala Ala  
915 920 925

gcc atc ttc ttg cca ctg gtg gcg atg gtg ttg gta gga ggt gta 3009  
Ala Ile Phe Leu Pro Leu Val Ala Met Val Leu Leu Val Gly Gly Val  
930 935 940

tac ttc tac ttc tcc agg ctc cag gga aaa agc tcc ctg cag ctg ccc 3057  
Tyr Phe Tyr Phe Ser Arg Leu Gln Gly Lys Ser Ser Leu Gln Leu Pro  
945 950 955 960

cgc ccc cgc ccc cgc ccc tac aac cgc att acc ata gag tca gcg ttt 3105  
Arg Pro Arg Pro Arg Pro Tyr Asn Arg Ile Thr Ile Glu Ser Ala Phe  
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gac aat cca act tac gag act gga tct ctt tcc ttt gca gga gac gag 3153  
Asp Asn Pro Thr Tyr Glu Thr Gly Ser Leu Ser Phe Ala Gly Asp Glu  
980 985 990

aga ata tgaagtctcc atctagggtgg gggcagtcata gggaaagtcaa ctcagacttg 3209  
Arg Ile

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caccttaggag gagatgccac caagccctca agaagttgtc ccctccccg cttgcgtatgc 3329

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<213> Homo sapiens

<223> n 1755 can be A, G, C, or T.

<400> 16

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20 25 30

Pro Gly Ile Glu Glu Thr Asp Gly Glu Leu Thr Ala Ala Pro Thr Pro  
35 40 45

Glu Gln Pro Glu Arg Gly Val His Phe Val Thr Thr Ala Pro Thr Leu  
50 55 60

Lys Leu Leu Asn His His Pro Leu Leu Glu Phe Leu Gln Glu Gly  
65 70 75 80

Leu Glu Lys Gly Asp Glu Glu Leu Arg Pro Ala Leu Pro Phe Gln Pro  
85 90 95

Asp Pro Pro Ala Pro Phe Thr Pro Ser Pro Leu Pro Arg Leu Ala Asn  
100 105 110

Gln Asp Ser Arg Pro Val Phe Thr Ser Pro Thr Pro Ala Met Ala Ala  
115 120 125

Val Pro Thr Gln Pro Gln Ser Lys Glu Gly Pro Trp Ser Pro Glu Ser  
130 135 140

Glu Ser Pro Met Leu Arg Ile Thr Ala Pro Leu Pro Pro Gly Pro Ser  
145 150 155 160

Met Ala Val Pro Thr Leu Gly Pro Gly Glu Ile Ala Ser Thr Thr Pro  
165 170 175

Pro Ser Arg Ala Trp Thr Pro Thr Gln Glu Gly Pro Gly Asp Met Gly  
180 185 190

Arg Pro Trp Val Ala Glu Val Val Ser Gln Gly Ala Gly Ile Gly Ile  
195 200 205

Gln Gly Thr Ile Thr Ser Ser Thr Ala Ser Gly Asp Asp Glu Glu Thr  
210 215 220

Thr Thr Thr Thr Ile Ile Thr Thr Thr Ile Thr Thr Val Gln Thr  
225 230 235 240

Pro Gly Pro Cys Ser Trp Asn Phe Ser Gly Pro Glu Gly Ser Leu Asp  
245 250 255

Ser Pro Thr Asp Leu Ser Ser Pro Thr Asp Val Gly Leu Asp Cys Phe  
260 265 270

Phe Tyr Ile Ser Val Tyr Pro Gly Tyr Gly Val Glu Ile Lys Val Gln  
275            280            285

Asn Ile Ser Leu Arg Glu Gly Glu Thr Val Thr Val Glu Gly Leu Gly  
290            295            300

Gly Pro Asp Pro Leu Pro Leu Ala Asn Gln Ser Phe Leu Leu Arg Gly  
305            310            315            320

Gln Val Ile Arg Ser Pro Thr His Gln Ala Ala Leu Arg Phe Gln Ser  
325            330            335

Leu Pro Pro Pro Ala Gly Pro Gly Thr Phe His Phe His Tyr Gln Ala  
340            345            350

Tyr Leu Leu Ser Cys His Phe Pro Arg Arg Gln Ala Tyr Glu Asp Val  
355            360            365

Thr Val Thr Ser Ile His Pro Gly Gly Ser Ala Arg Phe His Cys Ala  
370            375            380

Thr Gly Tyr Gln Leu Lys Gly Ala Arg His Leu Thr Cys Leu Asn Ala  
385            390            395            400

Thr Gln Pro Ile Trp Asp Ser Lys Glu Pro Val Cys Ile Ala Ala Cys  
405            410            415

Gly Gly Val Ile Arg Asn Ala Thr Thr Gly Arg Ile Val Ser Pro Gly  
420            425            430

Phe Pro Gly Asn Tyr Ser Asn Asn Leu Thr Cys His Trp Leu Leu Glu  
435            440            445

Ala Pro Glu Gly Gln Arg Leu His Leu His Phe Glu Lys Val Ser Leu  
450            455            460

Ala Glu Asp Asp Asp Arg Leu Ile Ile Arg Asn Gly Asp Asn Val Glu  
465            470            475            480

Ala Pro Pro Val Tyr Asp Ser Tyr Glu Val Glu Tyr Leu Pro Ile Glu  
485            490            495

Gly Leu Leu Ser Ser Gly Lys His Phe Phe Val Glu Leu Ser Thr Asp  
500            505            510

Ser Ser Gly Ala Ala Ala Gly Met Ala Leu Arg Tyr Glu Ala Phe Gln  
515            520            525

Gln Gly His Cys Tyr Glu Pro Phe Val Lys Tyr Gly Asn Phe Ser Ser  
530            535            540

Ser Thr Pro Thr Tyr Pro Val Gly Thr Thr Val Glu Phe Ser Cys Asp

545            550            555            560  
Pro Gly Tyr Thr Leu Glu Gln Gly Ser Ile Ile Ile Glu Cys Val Asp  
565            570            575  
Pro His Asp Pro Gln Trp Asn Glu Thr Glu Pro Ala Cys Arg Ala Val  
580            585            590  
Cys Ser Gly Glu Ile Thr Asp Ser Ala Gly Val Val Leu Ser Pro Asn  
595            600            605  
Trp Pro Glu Pro Tyr Ser Arg Gly Gln Asp Cys Ile Trp Gly Val His  
610            615            620  
Val Glu Glu Asp Lys Arg Ile Met Leu Asp Ile Arg Val Leu Arg Ile  
625            630            635            640  
Gly Pro Gly Asp Val Leu Thr Phe Tyr Asp Gly Asp Asp Leu Thr Ala  
645            650            655  
Arg Val Leu Gly Gln Tyr Ser Gly Pro Arg Ser His Phe Lys Leu Phe  
660            665            670  
Thr Ser Met Ala Asp Val Thr Ile Gln Phe Gln Ser Asp Pro Gly Thr  
675            680            685  
Ser Val Leu Gly Tyr Gln Gln Gly Phe Val Ile His Phe Phe Glu Val  
690            695            700  
Pro Arg Asn Asp Thr Cys Pro Glu Leu Pro Glu Ile Pro Asn Gly Trp  
705            710            715            720  
Lys Ser Pro Ser Gin Pro Glu Leu Val His Gly Thr Val Val Thr Tyr  
725            730            735  
Gln Cys Tyr Pro Gly Tyr Gln Val Val Gly Ser Ser Val Leu Met Cys  
740            745            750  
Gln Trp Asp Leu Thr Trp Ser Glu Asp Leu Pro Ser Cys Gln Arg Val  
755            760            765  
Thr Ser Cys His Asp Pro Gly Asp Val Glu His Ser Arg Arg Leu Ile  
770            775            780  
Ser Ser Pro Lys Phe Pro Val Gly Ala Thr Val Gln Tyr Ile Cys Asp  
785            790            795            800  
Gln Gly Phe Val Leu Thr Gly Ser Ser Ile Leu Thr Cys His Asp Arg  
805            810            815  
Gln Ala Gly Ser Pro Lys Trp Ser Asp Arg Ala Pro Lys Cys Leu Leu  
820            825            830

Glu Gln Leu Lys Pro Cys His Gly Leu Ser Ala Pro Glu Asn Gly Ala  
835            840            845

Arg Ser Pro Glu Lys Gln Leu His Pro Ala Gly Ala Thr Ile His Phe  
850            855            860

Ser Cys Ala Pro Gly Tyr Val Leu Lys Gly Gln Ala Ser Ile Lys Cys  
865            870            875            880

Val Pro Gly His Pro Ser His Trp Ser Asp Pro Pro Pro Ile Cys Arg  
885            890            895

Ala Ala Ser Leu Asp Gly Phe Tyr Asn Ser Arg Ser Leu Asp Val Ala  
900            905            910

Lys Ala Pro Ala Ala Ser Ser Thr Leu Asp Ala Ala His Ile Ala Ala  
915            920            925

Ala Ile Phe Leu Pro Leu Val Ala Met Val Leu Leu Val Gly Gly Val  
930            935            940

Tyr Phe Tyr Phe Ser Arg Leu Gln Gly Lys Ser Ser Leu Gln Leu Pro  
945            950            955            960

Arg Pro Arg Pro Arg Pro Tyr Asn Arg Ile Thr Ile Glu Ser Ala Phe  
965            970            975

Asp Asn Pro Thr Tyr Glu Thr Gly Ser Leu Ser Phe Ala Gly Asp Glu  
980            985            990

Arg Ile

<210> 17  
<211> 2127  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (178)..(1752)

<220>  
<223> n 2077 can be A, G, C, or T.

<400> 17  
ccaggcgctg gccgtggtgc tgattctgtc aggcgcgtggc ggcggcagcg gcggtgacgg 60  
ctgcggcccc gctccctcta cccggccgga cccggctctg ccccccgcgc caagccccac 120  
caagcccccc gccctcccgc cgccgtccca gcccaggcg cgcccgcaac cagcacc 177

atg cgc ccg gta gcc ctg ctg ctc ctg ccc tcg ctg gcg ctc ctg 225  
Met Arg Pro Val Ala Leu Leu Leu Leu Pro Ser Leu Leu Ala Leu Leu  
1 5 10 15

gct cac gga ctc tct tta gag gcc cca acc gtg ggg aaa gga caa gcc 273  
Ala His Gly Leu Ser Leu Glu Ala Pro Thr Val Gly Lys Gly Gln Ala  
20 25 30

cca ggc atc gag gag aca gat ggc gag ctg aca gca gcc ccc aca cct 321  
Pro Gly Ile Glu Glu Thr Asp Gly Glu Leu Thr Ala Ala Pro Thr Pro  
35 40 45

gag cag cca gaa cga ggc gtc cac ttt gtc aca aca gcc ccc acc ttg 369  
Glu Gln Pro Glu Arg Gly Val His Phe Val Thr Thr Ala Pro Thr Leu  
50 55 60

aag ctg ctc aac cac cac ccg ctg ctt gag gaa ttc cta caa gag ggg 417  
Lys Leu Leu Asn His His Pro Leu Leu Glu Glu Phe Leu Gln Glu Gly  
65 70 75 80

ctg gaa aag gga gat gag gag ctg agg cca gca ctg ccc ttc cag cct 465  
Leu Glu Lys Gly Asp Glu Glu Leu Arg Pro Ala Leu Pro Phe Gln Pro  
85 90 95

gac cca cct gca ccc ttc acc cca agt ccc ctt ccc cgc ctg gcc aac 513  
Asp Pro Pro Ala Pro Phe Thr Pro Ser Pro Leu Pro Arg Leu Ala Asn  
100 105 110

cag gac agc cgc cct gtc ttt acc agc ccc act cca gcc atg gct gcg 561  
Gln Asp Ser Arg Pro Val Phe Thr Ser Pro Thr Pro Ala Met Ala Ala  
115 120 125

gta ccc act cag ccc cag tcc aag gag gga ccc tgg agt ccg gag tca 609  
Val Pro Thr Gln Pro Gln Ser Lys Glu Gly Pro Trp Ser Pro Glu Ser  
130 135 140

gag tcc cct atg ctt cga atc aca gct ccc cta cct cca ggg ccc agc 657  
Glu Ser Pro Met Leu Arg Ile Thr Ala Pro Leu Pro Pro Gly Pro Ser  
145 150 155 160

atg gca gtg ccc acc cta ggc cca ggg gag ata gcc agc act aca ccc 705  
Met Ala Val Pro Thr Leu Gly Pro Gly Glu Ile Ala Ser Thr Thr Pro  
165 170 175

ccc agc aga gcc tgg aca cca acc caa gag ggt cct gga gac atg gga 753  
Pro Ser Arg Ala Trp Thr Pro Thr Gln Glu Gly Pro Gly Asp Met Gly  
180 185 190

agg ccg tgg gtt gca gag gtt gtg tcc cag ggc gca ggg atc ggg atc 801  
Arg Pro Trp Val Ala Glu Val Val Ser Gln Gly Ala Gly Ile Gly Ile  
195 200 205

cag ggg acc atc acc tcc tcc aca gct tca gga gat gat gag gag acc 849  
Gln Gly Thr Ile Thr Ser Ser Thr Ala Ser Gly Asp Asp Glu Glu Thr  
210 215 220

acc act acc acc atc atc acc acc aca gtc cag aca 897  
Thr Thr Thr Thr Ile Ile Thr Thr Thr Ile Thr Thr Val Gln Thr  
225 230 235 240

cca ggc cct tgt agc tgg aat ttc tca ggc cca gag ggc tct ctg gac 945  
Pro Gly Pro Cys Ser Trp Asn Phe Ser Gly Pro Glu Gly Ser Leu Asp  
245 250 255

tcc cct aca gac ctc agc tcc ccc act gat gtt ggc ctg gac tgc ttc 993  
Ser Pro Thr Asp Leu Ser Ser Pro Thr Asp Val Gly Leu Asp Cys Phe  
260 265 270

ttc tac atc tct gtc tac cct ggc tat ggc gtg gaa atc aag gtc cag 1041  
Phe Tyr Ile Ser Val Tyr Pro Gly Tyr Gly Val Glu Ile Lys Val Gln  
275 280 285

aat atc agc ctc cgg gaa ggg gag aca gtg act gtg gaa ggc ctg ggg 1089  
Asn Ile Ser Leu Arg Glu Gly Glu Thr Val Thr Val Glu Gly Leu Gly  
290 295 300

ggg cct gac cca ctg ccc ctg gcc aac cag tct ttc ctg ctg cgg ggc 1137  
Gly Pro Asp Pro Leu Pro Leu Ala Asn Gln Ser Phe Leu Leu Arg Gly  
305 310 315 320

caa gtc atc cgc agc ccc acc cac caa gcg gcc ctg agg ttc cag agc 1185  
Gln Val Ile Arg Ser Pro Thr His Gln Ala Ala Leu Arg Phe Gln Ser  
325 330 335

ctc ccg cca ccg gct ggc cct ggc acc ttc cat ttc cat tac caa gcc 1233  
Leu Pro Pro Pro Ala Gly Pro Gly Thr Phe His Phe His Tyr Gln Ala  
340 345 350

tat ctc ctg agc tgc cac ttt ccc cgt cgt cca gct tat gga gat gtg 1281  
Tyr Leu Leu Ser Cys His Phe Pro Arg Arg Pro Ala Tyr Gly Asp Val  
355 360 365

act gtc acc agc ctc cac cca ggg ggt agt gcc cgc ttc cat tgt gcc 1329  
Thr Val Thr Ser Leu His Pro Gly Gly Ser Ala Arg Phe His Cys Ala  
370 375 380

act ggc tac cag ctg aag ggc gcc agg cat ctc acc tgt ctc aat gcc 1377  
Thr Gly Tyr Gln Leu Lys Gly Ala Arg His Leu Thr Cys Leu Asn Ala  
385 390 395 400

acc cag ccc ttc tgg gat tca aag gag ccc gtc tgc atc gct gct tgc 1425  
Thr Gln Pro Phe Trp Asp Ser Lys Glu Pro Val Cys Ile Ala Ala Cys  
405 410 415

ggc gga gtg atc cgc aat ggc acc acc ggc cgc atc gtc tct cca ggc 1473

Gly Gly Val Ile Arg Asn Gly Thr Thr Gly Arg Ile Val Ser Pro Gly  
420 425 430

ttc ccg ggc aac tac agc aac ctc acc tgg cac tct gag 1521  
Phe Pro Gly Asn Tyr Ser Asn Asn Leu Thr Cys His Trp Leu Leu Glu  
435 440 445

gct cct gag ggc cag cggtt cta cac ctg cac ttt gag aag gtt tcc ctg 1569  
Ala Pro Glu Gly Gln Arg Leu His Leu His Phe Glu Lys Val Ser Leu  
450 455 460

gca gag gat gat gac agg ctc atc att cgc aat ggg gac aac gtg gag 1617  
Ala Glu Asp Asp Asp Arg Leu Ile Ile Arg Asn Gly Asp Asn Val Glu  
465 470 475 480

gcc cca cca gtg gga aaa agc tcc ctg cag ctg ccc cgc ccc ccc 1665  
Ala Pro Pro Val Gly Lys Ser Ser Leu Gln Leu Pro Arg Pro Arg Pro  
485 490 495

cgc ccc tac aac cgc att acc ata gag tca gcg ttt gac aat cca act 1713  
Arg Pro Tyr Asn Arg Ile Thr Ile Glu Ser Ala Phe Asp Asn Pro Thr  
500 505 510

tac gag act gga gag acg aga gaa tat gaa gtc tcc atc taggtgggg 1762  
Tyr Glu Thr Gly Glu Thr Arg Glu Tyr Glu Val Ser Ile  
515 520 525

cagtctaggg aagtcaactc agacttgcac cacagtccag cagcaaggct cttgtttcc 1822

tgctgtccct ccaccccttg tatataccac cttaggaggat atgccaccaa gcccctaaga 1882

agttgtgccc ttccccgcct gcgtgcacccatggccata tttcttggt gtcattgccc 1942

acttggggcc ctgcattgg gccatgtaca gggggcatct acctgtgggg aagaacatag 2002

ctgggagcac aagcttcaac agccagcatt cttgagcct cttcatggc cttgggacca 2062

gcctgggaa cacanttagg caggagcagg gagttacctt gttcacatg accaccaacc 2122

attcc 2127

<210> 18

<211> 525

<212> PRT

<213> Homo sapiens

<223> n 2077 can be A, G, C, or T.

<400> 18

Met Arg Pro Val Ala Leu Leu Leu Leu Pro Ser Leu Leu Ala Leu Leu  
1 5 10 15

Ala His Gly Leu Ser Leu Glu Ala Pro Thr Val Gly Lys Gly Gln Ala

20            25            30  
Pro Gly Ile Glu Glu Thr Asp Gly Glu Leu Thr Ala Ala Pro Thr Pro  
35            40            45  
Glu Gln Pro Glu Arg Gly Val His Phe Val Thr Thr Ala Pro Thr Leu  
50            55            60  
Lys Leu Leu Asn His His Pro Leu Leu Glu Phe Leu Gln Glu Gly  
65            70            75            80  
Leu Glu Lys Gly Asp Glu Glu Leu Arg Pro Ala Leu Pro Phe Gln Pro  
85            90            95  
Asp Pro Pro Ala Pro Phe Thr Pro Ser Pro Leu Pro Arg Leu Ala Asn  
100            105            110  
Gln Asp Ser Arg Pro Val Phe Thr Ser Pro Thr Pro Ala Met Ala Ala  
115            120            125  
Val Pro Thr Gln Pro Gln Ser Lys Glu Gly Pro Trp Ser Pro Glu Ser  
130            135            140  
Glu Ser Pro Met Leu Arg Ile Thr Ala Pro Leu Pro Pro Gly Pro Ser  
145            150            155            160  
Met Ala Val Pro Thr Leu Gly Pro Gly Glu Ile Ala Ser Thr Thr Pro  
165            170            175  
Pro Ser Arg Ala Trp Thr Pro Thr Gln Glu Gly Pro Gly Asp Met Gly  
180            185            190  
Arg Pro Trp Val Ala Glu Val Val Ser Gln Gly Ala Gly Ile Gly Ile  
195            200            205  
Gln Gly Thr Ile Thr Ser Ser Thr Ala Ser Gly Asp Asp Glu Glu Thr  
210            215            220  
Thr Thr Thr Thr Ile Ile Thr Thr Ile Thr Thr Val Gln Thr  
225            230            235            240  
Pro Gly Pro Cys Ser Trp Asn Phe Ser Gly Pro Glu Gly Ser Leu Asp  
245            250            255  
Ser Pro Thr Asp Leu Ser Ser Pro Thr Asp Val Gly Leu Asp Cys Phe  
260            265            270  
Phe Tyr Ile Ser Val Tyr Pro Gly Tyr Gly Val Glu Ile Lys Val Gln  
275            280            285  
Asn Ile Ser Leu Arg Glu Gly Glu Thr Val Thr Val Glu Gly Leu Gly  
290            295            300

Gly Pro Asp Pro Leu Pro Leu Ala Asn Gln Ser Phe Leu Leu Arg Gly  
305            310            315            320

Gln Val Ile Arg Ser Pro Thr His Gln Ala Ala Leu Arg Phe Gln Ser  
325            330            335

Leu Pro Pro Pro Ala Gly Pro Gly Thr Phe His Phe His Tyr Gln Ala  
340            345            350

Tyr Leu Leu Ser Cys His Phe Pro Arg Arg Pro Ala Tyr Gly Asp Val  
355            360            365

Thr Val Thr Ser Leu His Pro Gly Gly Ser Ala Arg Phe His Cys Ala  
370            375            380

Thr Gly Tyr Gln Leu Lys Gly Ala Arg His Leu Thr Cys Leu Asn Ala  
385            390            395            400

Thr Gln Pro Phe Trp Asp Ser Lys Glu Pro Val Cys Ile Ala Ala Cys  
405            410            415

Gly Gly Val Ile Arg Asn Gly Thr Thr Gly Arg Ile Val Ser Pro Gly  
420            425            430

Phe Pro Gly Asn Tyr Ser Asn Asn Leu Thr Cys His Trp Leu Leu Glu  
435            440            445

Ala Pro Glu Gly Gln Arg Leu His Leu His Phe Glu Lys Val Ser Leu  
450            455            460

Ala Glu Asp Asp Asp Arg Leu Ile Ile Arg Asn Gly Asp Asn Val Glu  
465            470            475            480

Ala Pro Pro Val Gly Lys Ser Ser Leu Gln Leu Pro Arg Pro Arg Pro  
485            490            495

Arg Pro Tyr Asn Arg Ile Thr Ile Glu Ser Ala Phe Asp Asn Pro Thr  
500            505            510

Tyr Glu Thr Gly Glu Thr Arg Glu Tyr Glu Val Ser Ile  
515            520            525

<210> 19  
<211> 2127  
<212> DNA  
<213> Homo sapiens  
  
<220>  
<221> CDS  
<222> (178)..(1752)

<220>

<223> n 2077 can be A, G, C, or T.

<400> 19

ccaggcgctg gccgtggtgc tgattctgtc aggcgctggc ggccggcagcg gcgggtacgg 60

ctgcggcccc gctccctcta cccggccgga cccggctctg ccccccgcac caagccccac 120

caagcccccc gccctcccgc cgccgtccca gcccagggcg cggccgcaac cagcacc 177

atg cgc ccg gta gcc ctg ctg ctc ctg ccc tcg ctg gcg ctc ctg 225

Met Arg Pro Val Ala Leu Leu Leu Pro Ser Leu Leu Ala Leu Leu

1 5 10 15

gct cac gga ctc tct tta gag gcc cca acc gtg ggg aaa gga caa gcc 273

Ala His Gly Leu Ser Leu Glu Ala Pro Thr Val Gly Lys Gly Gln Ala

20 25 30

cca ggc atc gag gag aca gat ggc gag ctg aca gca gcc ccc aca cct 321

Pro Gly Ile Glu Glu Thr Asp Gly Glu Leu Thr Ala Ala Pro Thr Pro

35 40 45

gag cag cca gaa cga ggc gtc cac ttt gtc aca aca gcc ccc acc ttg 369

Glu Gln Pro Glu Arg Gly Val His Phe Val Thr Thr Ala Pro Thr Leu

50 55 60

aag ctg ctc aac cac cac ccg ctg ctt gag gaa ttc cta caa gag ggg 417

Lys Leu Leu Asn His His Pro Leu Leu Glu Glu Phe Leu Gln Glu Gly

65 70 75 80

ctg gaa aag gga gat gag gag ctg agg cca gca ctg ccc ttc cag cct 465

Leu Glu Lys Gly Asp Glu Glu Leu Arg Pro Ala Leu Pro Phe Gln Pro

85 90 95

gac cca cct gca ccc ttc acc cca agt ccc ctt ccc cgc ctg gcc aac 513

Asp Pro Pro Ala Pro Phe Thr Pro Ser Pro Leu Pro Arg Leu Ala Asn

100 105 110

cag gac agc cgc cct gtc ttt acc agc ccc act cca gcc atg gct gcg 561

Gln Asp Ser Arg Pro Val Phe Thr Ser Pro Thr Pro Ala Met Ala Ala

115 120 125

gta ccc act cag ccc cag tcc aag gag gga ccc tgg agt ccg gag tca 609

Val Pro Thr Gln Pro Gln Ser Lys Glu Gly Pro Trp Ser Pro Glu Ser

130 135 140

gag tcc cct atg ctt cga atc aca gct ccc cta cct cca ggg ccc agc 657

Glu Ser Pro Met Leu Arg Ile Thr Ala Pro Leu Pro Pro Gly Pro Ser

145 150 155 160

atg gca gtg ccc acc cta ggc cca ggg gag ata gcc agc act aca ccc 705

Met Ala Val Pro Thr Leu Gly Pro Gly Glu Ile Ala Ser Thr Thr Pro

165 170 175

ccc agc aga gcc tgg aca cca acc caa gag ggt cct gga gac atg gga 753  
Pro Ser Arg Ala Trp Thr Pro Thr Gln Glu Gly Pro Gly Asp Met Gly  
180 185 190

agg ccg tgg gtt gca gag gtt gtg tcc cag ggc gca ggg atc ggg atc 801  
Arg Pro Trp Val Ala Glu Val Val Ser Gln Gly Ala Gly Ile Gly Ile  
195 200 205

cag ggg acc atc acc tcc tcc aca gct tca gga gat gat gag gag acc 849  
Gln Gly Thr Ile Thr Ser Ser Thr Ala Ser Gly Asp Asp Glu Glu Thr  
210 215 220

acc act acc acc acc atc acc acc acc atc acc aca gtc cag aca 897  
Thr Thr Thr Thr Ile Ile Thr Thr Thr Ile Thr Val Gln Thr  
225 230 235 240

cca ggc cct tgt agc tgg aat ttc tca ggc cca gag ggc tct ctg gac 945  
Pro Gly Pro Cys Ser Trp Asn Phe Ser Gly Pro Glu Gly Ser Leu Asp  
245 250 255

tcc cct aca gac ctc agc tcc ccc act gat gtt ggc ctg gac tgc ttc 993  
Ser Pro Thr Asp Leu Ser Ser Pro Thr Asp Val Gly Leu Asp Cys Phe  
260 265 270

ttc tac atc tct gtc tac cct ggc tat ggc gtg gaa atc aag gtc cag 1041  
Phe Tyr Ile Ser Val Tyr Pro Gly Tyr Gly Val Glu Ile Lys Val Gln  
275 280 285

aat atc agc ctc cg<sup>g</sup> gaa ggg gag aca gtg act gtg gaa ggc ctg ggg 1089  
Asn Ile Ser Leu Arg Glu Gly Glu Thr Val Thr Val Glu Gly Leu Gly  
290 295 300

ggg cct gac cca ctg ccc ctg gcc aac cag tct ttc ctg ctg cgg ggc 1137  
Gly Pro Asp Pro Leu Pro Leu Ala Asn Gln Ser Phe Leu Leu Arg Gly  
305 310 315 320

caa gtc atc cgc agc ccc acc cac caa gcg gcc ctg agg ttc cag agc 1185  
Gln Val Ile Arg Ser Pro Thr His Gln Ala Ala Leu Arg Phe Gln Ser  
325 330 335

ctc ccg cca ccg gct ggc cct ggc acc ttc cat ttc cat tac caa gcc 1233  
Leu Pro Pro Pro Ala Gly Pro Gly Thr Phe His Phe His Tyr Gln Ala  
340 345 350

tat ctc ctg agc tgc cac ttt ccc cgt cgt cca gct tat gga gat gtg 1281  
Tyr Leu Leu Ser Cys His Phe Pro Arg Arg Pro Ala Tyr Gly Asp Val  
355 360 365

act gtc acc agc ctc cac cca ggg ggt agt gcc cgc ttc cat tgt gcc 1329  
Thr Val Thr Ser Leu His Pro Gly Gly Ser Ala Arg Phe His Cys Ala  
370 375 380

act ggc tac cag ctg aag ggc gcc agg cat ctc acc tgt ctc aat gcc 1377  
Thr Gly Tyr Gln Leu Lys Gly Ala Arg His Leu Thr Cys Leu Asn Ala  
385 390 395 400

acc cag ccc ttc tgg gat tca aag gag ccc gtc tgc atc gct gtc 1425  
Thr Gln Pro Phe Trp Asp Ser Lys Glu Pro Val Cys Ile Ala Ala Cys  
405 410 415

ggc gga gtg atc cgc aat ggc acc acc ggc cgc atc gtc tct cca ggc 1473  
Gly Gly Val Ile Arg Asn Gly Thr Thr Gly Arg Ile Val Ser Pro Gly  
420 425 430

ttc ccg ggc aac tac agc aac aac ctc acc tgt cac tgg ctg ctt gag 1521  
Phe Pro Gly Asn Tyr Ser Asn Asn Leu Thr Cys His Trp Leu Leu Glu  
435 440 445

gct cct gag ggc cag cgg cta cac ctg cac ttt gag aag gtt tcc ctg 1569  
Ala Pro Glu Gly Gln Arg Leu His Leu His Phe Glu Lys Val Ser Leu  
450 455 460

gca gag gat gat gac agg ctc atc att cgc aat ggg gac aac gtg gag 1617  
Ala Glu Asp Asp Asp Arg Leu Ile Ile Arg Asn Gly Asp Asn Val Glu  
465 470 475 480

gcc cca cca gtg tat gat tcc tat gag gtg gaa tac ccg ccc cgc ccc 1665  
Ala Pro Pro Val Tyr Asp Ser Tyr Glu Val Glu Tyr Pro Pro Arg Pro  
485 490 495

cgc ccc tac aac cgc att acc ata gag tca gcg ttt gac aat cca act 1713  
Arg Pro Tyr Asn Arg Ile Thr Ile Glu Ser Ala Phe Asp Asn Pro Thr  
500 505 510

tac gag act gga gag acg aga gaa tat gaa gtc tcc atc taggtgggg 1762  
Tyr Glu Thr Gly Glu Thr Arg Glu Tyr Glu Val Ser Ile  
515 520 525

cagtctaggg aagtcaactc agacttgcac cacagtccag cagcaaggct cttgtttcc 1822

tgctgtccct ccacctctg tatataccac ctaggaggag atgccaccaa gccctaaga 1882

agtttgtccc ttccccgct gcgatgccc ccatggctt tttcttggt gtcattgccc 1942

acttggggcc cttgcattgg gccatgtaca gggggcatct acctgtgggg aagaacatag 2002

ctgggagcac aagctcaac agccagcatt cttgagcct cttcatggc cctgggacca 2062

gcctggggaa cacanttagg caggagcagg gagttacctt gttcacatg accaccaacc 2122

attcc 2127

<210> 20

<211> 525

<212> PRT

<213> Homo sapiens

<223> n 2077 can be A, G, C, or T.

<400> 20

Met Arg Pro Val Ala Leu Leu Leu Leu Pro Ser Leu Leu Ala Leu Leu  
1 5 10 15

Ala His Gly Leu Ser Leu Glu Ala Pro Thr Val Gly Lys Gly Gln Ala  
20 25 30

Pro Gly Ile Glu Glu Thr Asp Gly Glu Leu Thr Ala Ala Pro Thr Pro  
35 40 45

Glu Gln Pro Glu Arg Gly Val His Phe Val Thr Thr Ala Pro Thr Leu  
50 55 60

Lys Leu Leu Asn His His Pro Leu Leu Glu Glu Phe Leu Gln Glu Gly  
65 70 75 80

Leu Glu Lys Gly Asp Glu Glu Leu Arg Pro Ala Leu Pro Phe Gln Pro  
85 90 95

Asp Pro Pro Ala Pro Phe Thr Pro Ser Pro Leu Pro Arg Leu Ala Asn  
100 105 110

Gln Asp Ser Arg Pro Val Phe Thr Ser Pro Thr Pro Ala Met Ala Ala  
115 120 125

Val Pro Thr Gln Pro Gln Ser Lys Glu Gly Pro Trp Ser Pro Glu Ser  
130 135 140

Glu Ser Pro Met Leu Arg Ile Thr Ala Pro Leu Pro Pro Gly Pro Ser  
145 150 155 160

Met Ala Val Pro Thr Leu Gly Pro Gly Glu Ile Ala Ser Thr Thr Pro  
165 170 175

Pro Ser Arg Ala Trp Thr Pro Thr Gln Glu Gly Pro Gly Asp Met Gly  
180 185 190

Arg Pro Trp Val Ala Glu Val Val Ser Gln Gly Ala Gly Ile Gly Ile  
195 200 205

Gln Gly Thr Ile Thr Ser Ser Thr Ala Ser Gly Asp Asp Glu Glu Thr  
210 215 220

Thr Thr Thr Thr Ile Ile Thr Thr Thr Ile Thr Thr Val Gln Thr  
225 230 235 240

Pro Gly Pro Cys Ser Trp Asn Phe Ser Gly Pro Glu Gly Ser Leu Asp  
245 250 255

Ser Pro Thr Asp Leu Ser Ser Pro Thr Asp Val Gly Leu Asp Cys Phe  
260                265                270

Phe Tyr Ile Ser Val Tyr Pro Gly Tyr Gly Val Glu Ile Lys Val Gln  
275                280                285

Asn Ile Ser Leu Arg Glu Gly Glu Thr Val Thr Val Glu Gly Leu Gly  
290                295                300

Gly Pro Asp Pro Leu Pro Leu Ala Asn Gln Ser Phe Leu Leu Arg Gly  
305                310                315                320

Gln Val Ile Arg Ser Pro Thr His Gln Ala Ala Leu Arg Phe Gln Ser  
325                330                335

Leu Pro Pro Pro Ala Gly Pro Gly Thr Phe His His Tyr Gln Ala  
340                345                350

Tyr Leu Leu Ser Cys His Phe Pro Arg Arg Pro Ala Tyr Gly Asp Val  
355                360                365

Thr Val Thr Ser Leu His Pro Gly Gly Ser Ala Arg Phe His Cys Ala  
370                375                380

Thr Gly Tyr Gln Leu Lys Gly Ala Arg His Leu Thr Cys Leu Asn Ala  
385                390                395                400

Thr Gln Pro Phe Trp Asp Ser Lys Glu Pro Val Cys Ile Ala Ala Cys  
405                410                415

Gly Gly Val Ile Arg Asn Gly Thr Thr Gly Arg Ile Val Ser Pro Gly  
420                425                430

Phe Pro Gly Asn Tyr Ser Asn Asn Leu Thr Cys His Trp Leu Leu Glu  
435                440                445

Ala Pro Glu Gly Gln Arg Leu His Leu His Phe Glu Lys Val Ser Leu  
450                455                460

Ala Glu Asp Asp Asp Arg Leu Ile Ile Arg Asn Gly Asp Asn Val Glu  
465                470                475                480

Ala Pro Pro Val Tyr Asp Ser Tyr Glu Val Glu Tyr Pro Pro Arg Pro  
485                490                495

Arg Pro Tyr Asn Arg Ile Thr Ile Glu Ser Ala Phe Asp Asn Pro Thr  
500                505                510

Tyr Glu Thr Gly Glu Thr Arg Glu Tyr Glu Val Ser Ile  
515                520                525

<210> 21  
<211> 1988  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (178)..(1752)

<400> 21  
ccaggcgctg gccgtggtgc tgattctgtc aggcgctggc ggccggcagcg gcggtgacgg 60  
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caagcccccc gccctccgcg cgccggctcca gcccagggcg cggccgcaac cagcacc 177  
atg cgc ccg gta gcc ctg ctg ctc ctg ccc tcg ctg ctg gcg ctc ctg 225  
Met Arg Pro Val Ala Leu Leu Leu Pro Ser Leu Leu Ala Leu Leu  
1 5 10 15

gct cac gga ctc tct tta gag gcc cca acc gtg ggg aaa gga caa gcc 273  
Ala His Gly Leu Ser Leu Glu Ala Pro Thr Val Gly Lys Gly Gln Ala  
20 25 30

cca ggc atc gag gag aca gat ggc gag ctg aca gca gcc ccc aca cct 321  
Pro Gly Ile Glu Glu Thr Asp Gly Glu Leu Thr Ala Ala Pro Thr Pro  
35 40 45

gag cag cca gaa cga ggc gtc cac ttt gtc aca aca gcc ccc acc ttg 369  
Glu Gln Pro Glu Arg Gly Val His Phe Val Thr Thr Ala Pro Thr Leu  
50 55 60

aag ctg ctc aac cac cac ccg ctg ctt gag gaa ttc cta caa gag ggg 417  
Lys Leu Leu Asn His His Pro Leu Leu Glu Glu Phe Leu Gln Glu Gly  
65 70 75 80

ctg gaa aag gga gat gag gag ctg agg cca gca ctg ccc ttc cag cct 465  
Leu Glu Lys Gly Asp Glu Glu Leu Arg Pro Ala Leu Pro Phe Gln Pro  
85 90 95

gac cca cct gca ccc ttc acc cca agt ccc ctt ccc cgc ctg gcc aac 513  
Asp Pro Pro Ala Pro Phe Thr Pro Ser Pro Leu Pro Arg Leu Ala Asn  
100 105 110

cag gag agc cgc cct gtc ttt acc agc ccc act cca gcc atg gct gcg 561  
Gln Asp Ser Arg Pro Val Phe Thr Ser Pro Thr Pro Ala Met Ala Ala  
115 120 125

gta ccc act cag ccc cag tcc aag gag gga ccc tgg agt ccg gag tca 609  
Val Pro Thr Gln Pro Gln Ser Lys Glu Gly Pro Trp Ser Pro Glu Ser  
130 135 140

gag tcc cct atg ctt cga atc aca gct ccc cta cct cca ggg ccc agc 657

Glu Ser Pro Met Leu Arg Ile Thr Ala Pro Leu Pro Pro Gly Pro Ser  
145 150 155 160

atg gca gtg ccc acc cta ggc cca ggg gag ata gcc agc act aca ccc 705  
Met Ala Val Pro Thr Leu Gly Pro Gly Glu Ile Ala Ser Thr Thr Pro  
165 170 175

ccc agc aga gcc tgg aca cca acc caa gag ggt cct gga gac atg gga 753  
Pro Ser Arg Ala Trp Thr Pro Thr Gln Glu Gly Pro Gly Asp Met Gly  
180 185 190

agg ccg tgg gtt gca gag gtt gtg tcc cag ggc gca ggg atc ggg atc 801  
Arg Pro Trp Val Ala Glu Val Val Ser Gln Gly Ala Gly Ile Gly Ile  
195 200 205

cag ggg acc atc acc tcc tcc aca gct tca gga gat gat gag gag acc 849  
Gln Gly Thr Ile Thr Ser Ser Thr Ala Ser Gly Asp Asp Glu Glu Thr  
210 215 220

acc act acc acc acc atc acc acc acc atc acc aca gtc cag aca 897  
Thr Thr Thr Thr Ile Ile Thr Thr Ile Thr Val Gln Thr  
225 230 235 240

cca ggc cct tgt agc tgg aat ttc tca ggc cca gag ggc tct ctg gac 945  
Pro Gly Pro Cys Ser Trp Asn Phe Ser Gly Pro Glu Gly Ser Leu Asp  
245 250 255

tcc cct aca gac ctc agc tcc ccc act gat gtt ggc ctg gac tgc ttc 993  
Ser Pro Thr Asp Leu Ser Ser Pro Thr Asp Val Gly Leu Asp Cys Phe  
260 265 270

ttc tac atc tct gtc tac cct ggc tat ggc gtg gaa atc aag gtc cag 1041  
Phe Tyr Ile Ser Val Tyr Pro Gly Tyr Gly Val Glu Ile Lys Val Gln  
275 280 285

aat atc agc ctc cgg gaa ggg gag aca gtg act gtg gaa ggc ctg ggg 1089  
Asn Ile Ser Leu Arg Glu Gly Glu Thr Val Thr Val Glu Gly Leu Gly  
290 295 300

ggg cct gac cca ctg ccc ctg gcc aac cag tct ttc ctg ctg cgg ggc 1137  
Gly Pro Asp Pro Leu Pro Leu Ala Asn Gln Ser Phe Leu Leu Arg Gly  
305 310 315 320

caa gtc atc cgc agc ccc acc cac caa gcg gcc ctg agg ttc cag agc 1185  
Gln Val Ile Arg Ser Pro Thr His Gln Ala Ala Leu Arg Phe Gln Ser  
325 330 335

ctc ccg cca ccg gct ggc cct ggc acc ttc cat ttc cat tac caa gcc 1233  
Leu Pro Pro Ala Gly Pro Gly Thr Phe His Phe His Tyr Gln Ala  
340 345 350

tat ctc ctg agc tgc cac ttt ccc cgt cgt cca gct tat gga gat gtg 1281  
Tyr Leu Leu Ser Cys His Phe Pro Arg Arg Pro Ala Tyr Gly Asp Val

355

360

365

act gtc acc agc ctc cac cca ggg ggt agt gcc cgc ttc cat tgt gcc 1329  
Thr Val Thr Ser Leu His Pro Gly Gly Ser Ala Arg Phe His Cys Ala  
370 375 380

act ggc tac cag ctg aag ggc gcc agg cat ctc acc tgt ctc aat gcc 1377  
Thr Gly Tyr Gln Leu Lys Gly Ala Arg His Leu Thr Cys Leu Asn Ala  
385 390 395 400

acc cag ccc ttc tgg gat tca aag gag ccc gtc tgc atc gct gct tgc 1425  
Thr Gln Pro Phe Trp Asp Ser Lys Glu Pro Val Cys Ile Ala Ala Cys  
405 410 415

ggc gga gtg atc cgc aat ggc acc acc ggc cgc atc gtc tct cca ggc 1473  
Gly Gly Val Ile Arg Asn Gly Thr Thr Gly Arg Ile Val Ser Pro Gly  
420 425 430

tac ccg ggc aac tac agc aac aac ctc acc tgt cac tgg ctg ctt gag 1521  
Phe Pro Gly Asn Tyr Ser Asn Asn Leu Thr Cys His Trp Leu Leu Glu  
435 440 445

gct cct gag ggc cag cgg cta cac ctg cac ttt gag aag gtt tcc ctg 1569  
Ala Pro Glu Gly Gln Arg Leu His Leu His Phe Glu Lys Val Ser Leu  
450 455 460

gca gag gat gat gac agg ctc atc att cgc aat ggg gac aac gtg gag 1617  
Ala Glu Asp Asp Asp Arg Leu Ile Arg Asn Gly Asp Asn Val Glu  
465 470 475 480

gcc cca cca gtg tat gat tcc tat gag gtg gaa tac ccg ccc cgc ccc 1665  
Ala Pro Pro Val Tyr Asp Ser Tyr Glu Val Glu Tyr Pro Pro Arg Pro  
485 490 495

cgc ccc tac aac cgc att acc ata gag tca gcg ttt gac aat cca act 1713  
Arg Pro Tyr Asn Arg Ile Thr Ile Glu Ser Ala Phe Asp Asn Pro Thr  
500 505 510

tac gag act gga gag acg aga gaa tat gaa gtc tcc atc taggtgggg 1762  
Tyr Glu Thr Gly Glu Thr Arg Glu Tyr Glu Val Ser Ile  
515 520 525

cagtctaggg aagtcaactc agacttgcac cacagtccag cagcaaggct ccttgcttcc 1822

tgctgtccct ccacccctcg tatataccac ctaggaggag atgccaccaa gccacttgt 1882

acatgtaatg tattatatgg ggtctggct ccagccagag aacaatctt tatttctgtt 1942

gtttccttat taaaatggtg ttttggaaa aaaaaaaaaaaaaaaa 1988

<210> 22

<211> 525

<212> PRT

<213> Homo sapiens

<400> 22

Met Arg Pro Val Ala Leu Leu Leu Leu Pro Ser Leu Leu Ala Leu Leu  
1 5 10 15

Ala His Gly Leu Ser Leu Glu Ala Pro Thr Val Gly Lys Gly Gln Ala  
20 25 30

Pro Gly Ile Glu Glu Thr Asp Gly Glu Leu Thr Ala Ala Pro Thr Pro  
35 40 45

Glu Gln Pro Glu Arg Gly Val His Phe Val Thr Thr Ala Pro Thr Leu  
50 55 60

Lys Leu Leu Asn His His Pro Leu Leu Glu Glu Phe Leu Gln Glu Gly  
65 70 75 80

Leu Glu Lys Gly Asp Glu Glu Leu Arg Pro Ala Leu Pro Phe Gln Pro  
85 90 95

Asp Pro Pro Ala Pro Phe Thr Pro Ser Pro Leu Pro Arg Leu Ala Asn  
100 105 110

Gln Asp Ser Arg Pro Val Phe Thr Ser Pro Thr Pro Ala Met Ala Ala  
115 120 125

Val Pro Thr Gln Pro Gln Ser Lys Glu Gly Pro Trp Ser Pro Glu Ser  
130 135 140

Glu Ser Pro Met Leu Arg Ile Thr Ala Pro Leu Pro Pro Gly Pro Ser  
145 150 155 160

Met Ala Val Pro Thr Leu Gly Pro Gly Glu Ile Ala Ser Thr Thr Pro  
165 170 175

Pro Ser Arg Ala Trp Thr Pro Thr Gln Glu Gly Pro Gly Asp Met Gly  
180 185 190

Arg Pro Trp Val Ala Glu Val Val Ser Gln Gly Ala Gly Ile Gly Ile  
195 200 205

Gin Gly Thr Ile Thr Ser Ser Thr Ala Ser Gly Asp Asp Glu Glu Thr  
210 215 220

Thr Thr Thr Thr Ile Ile Thr Thr Thr Ile Thr Thr Val Gln Thr  
225 230 235 240

Pro Gly Pro Cys Ser Trp Asn Phe Ser Gly Pro Glu Gly Ser Leu Asp  
245 250 255

Ser Pro Thr Asp Leu Ser Ser Pro Thr Asp Val Gly Leu Asp Cys Phe

260

265

270

Phe Tyr Ile Ser Val Tyr Pro Gly Tyr Gly Val Glu Ile Lys Val Gln

275

280

285

Asn Ile Ser Leu Arg Glu Gly Glu Thr Val Thr Val Glu Gly Leu Gly

290

295

300

Gly Pro Asp Pro Leu Pro Leu Ala Asn Gln Ser Phe Leu Leu Arg Gly

305

310

315

320

Gln Val Ile Arg Ser Pro Thr His Gln Ala Ala Leu Arg Phe Gln Ser

325

330

335

Leu Pro Pro Pro Ala Gly Pro Gly Thr Phe His Phe His Tyr Gln Ala

340

345

350

Tyr Leu Leu Ser Cys His Phe Pro Arg Arg Pro Ala Tyr Gly Asp Val

355

360

365

Thr Val Thr Ser Leu His Pro Gly Gly Ser Ala Arg Phe His Cys Ala

370

375

380

Thr Gly Tyr Gln Leu Lys Gly Ala Arg His Leu Thr Cys Leu Asn Ala

385

390

395

400

Thr Gln Pro Phe Trp Asp Ser Lys Glu Pro Val Cys Ile Ala Ala Cys

405

410

415

Gly Gly Val Ile Arg Asn Gly Thr Thr Gly Arg Ile Val Ser Pro Gly

420

425

430

Phe Pro Gly Asn Tyr Ser Asn Asn Leu Thr Cys His Trp Leu Leu Glu

435

440

445

Ala Pro Glu Gly Gln Arg Leu His Leu His Phe Glu Lys Val Ser Leu

450

455

460

Ala Glu Asp Asp Asp Arg Leu Ile Ile Arg Asn Gly Asp Asn Val Glu

465

470

475

480

Ala Pro Pro Val Tyr Asp Ser Tyr Glu Val Glu Tyr Pro Pro Arg Pro

485

490

495

Arg Pro Tyr Asn Arg Ile Thr Ile Glu Ser Ala Phe Asp Asn Pro Thr

500

505

510

Tyr Glu Thr Gly Glu Thr Arg Glu Tyr Glu Val Ser Ile

515

520

525

<211> 2143  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (178)..(1755)

<220>  
<223> n 2093 can be A, G, C, or T.

<400> 23  
ccaggcgctgc gccgtggtgc tgattctgtc aggcgctggc ggccggcagcg gccgggtacgg 60  
ctgcggcccc gtcctctca cccggccgga cccggctctg ccccgccccc caagccccac 120  
caagcccccc gcccctccgc cgccgtccca gcccaggcg cggccgcaac cagcacc 177  
atg cgc ccg gta gcc ctg ctc ctg ccc tcg ctg ctg gcg ctc ctg 225  
Met Arg Pro Val Ala Leu Leu Leu Pro Ser Leu Leu Ala Leu Leu  
1 5 10 15  
gct cac gga ctc tct tta gag gcc cca acc gtg ggg aaa gga caa gcc 273  
Ala His Gly Leu Ser Leu Glu Ala Pro Thr Val Gly Lys Gly Gln Ala  
20 25 30  
cca ggc atc gag gag aca gat ggc gag ctg aca gca gcc ccc aca cct 321  
Pro Gly Ile Glu Glu Thr Asp Gly Glu Leu Thr Ala Ala Pro Thr Pro  
35 40 45  
gag cag cca gaa cga ggc gtc cac ttt gtc aca aca gcc ccc acc ttg 369  
Glu Gln Pro Glu Arg Gly Val His Phe Val Thr Thr Ala Pro Thr Leu  
50 55 60  
aag ctg ctc aac cac cac ccg ctg ctt gag gaa ttc cta caa gag ggg 417  
Lys Leu Leu Asn His His Pro Leu Leu Glu Glu Phe Leu Gln Glu Gly  
65 70 75 80  
ctg gaa aag gga gat gag gag ctg agg cca gca ctg ccc ttc cag cct 465  
Leu Glu Lys Gly Asp Glu Glu Leu Arg Pro Ala Leu Pro Phe Gln Pro  
85 90 95  
gac cca cct gca ccc ttc acc cca agt ccc ctt ccc cgc ctg gcc aac 513  
Asp Pro Pro Ala Pro Phe Thr Pro Ser Pro Leu Pro Arg Leu Ala Asn  
100 105 110  
cag gac agc cgc cct gtc ttt acc agc ccc act cca gcc atg gct gcg 561  
Gln Asp Ser Arg Pro Val Phe Thr Ser Pro Thr Pro Ala Met Ala Ala  
115 120 125  
gta ccc act cag ccc cag tcc aag gag gga ccc tgg agt ccg gag tca 609  
Val Pro Thr Gln Pro Gln Ser Lys Glu Gly Pro Trp Ser Pro Glu Ser  
130 135 140

gag tcc cct atg ctt cga atc aca gct ccc cta cct cca ggg ccc agc 657  
Glu Ser Pro Met Leu Arg Ile Thr Ala Pro Leu Pro Pro Gly Pro Ser  
145 150 155 160

atg gca gtg ccc acc cta ggc cca ggg gag ata gcc agc act aca ccc 705  
Met Ala Val Pro Thr Leu Gly Pro Gly Glu Ile Ala Ser Thr Thr Pro  
165 170 175

ccc agc aga gcc tgg aca cca acc caa gag ggt cct gga gac atg gga 753  
Pro Ser Arg Ala Trp Thr Pro Thr Gln Glu Gly Pro Gly Asp Met Gly  
180 185 190

agg ccg tgg gtt gca gag gtt gtg tcc cag ggc gca ggg atc ggg atc 801  
Arg Pro Trp Val Ala Glu Val Val Ser Gln Gly Ala Gly Ile Gly Ile  
195 200 205

cag ggg acc atc acc tcc tcc aca gct tca gga gat gat gag gag acc 849  
Gln Gly Thr Ile Thr Ser Ser Thr Ala Ser Gly Asp Asp Glu Glu Thr  
210 215 220

acc act acc acc acc atc atc acc acc atc acc aca gtc cag aca 897  
Thr Thr Thr Thr Ile Ile Thr Thr Thr Ile Thr Thr Val Gln Thr  
225 230 235 240

cca ggc cct tgt agc tgg aat ttc tca ggc cca gag ggc tct ctg gac 945  
Pro Gly Pro Cys Ser Trp Asn Phe Ser Gly Pro Glu Gly Ser Leu Asp  
245 250 255

tcc cct aca gac ctc agc tcc ccc act gat gtt ggc ctg gac tgc ttc 993  
Ser Pro Thr Asp Leu Ser Ser Pro Thr Asp Val Gly Leu Asp Cys Phe  
260 265 270

ttc tac atc tct gtc tac cct ggc tat ggc gtg gaa atc aag gtc cag 1041  
Phe Tyr Ile Ser Val Tyr Pro Gly Tyr Gly Val Glu Ile Lys Val Gln  
275 280 285

aat atc agc ctc cg<sup>g</sup> gaa ggg gag aca gtg act gtg gaa ggc ctg ggg 1089  
Asn Ile Ser Leu Arg Glu Gly Glu Thr Val Thr Val Glu Gly Leu Gly  
290 295 300

ggg cct gac cca ctg ccc ctg gcc aac cag tct ttc ctg ctg cgg ggc 1137  
Gly Pro Asp Pro Leu Pro Leu Ala Asn Gln Ser Phe Leu Leu Arg Gly  
305 310 315 320

caa gtc atc cgc agc ccc acc cac caa gcg gcc ctg agg ttc cag agc 1185  
Gln Val Ile Arg Ser Pro Thr His Gln Ala Ala Leu Arg Phe Gln Ser  
325 330 335

ctc ccg cca ccg gct ggc cct ggc acc ttc cat ttc cat tac caa gcc 1233  
Leu Pro Pro Ala Gly Pro Gly Thr Phe His Phe His Tyr Gln Ala  
340 345 350

tat ctc ctg agc tgc cac ttt ccc cgt cgt cca gct tat gga gat gtg 1281  
Tyr Leu Leu Ser Cys His Phe Pro Arg Arg Pro Ala Tyr Gly Asp Val  
355 360 365

act gtc acc agc ctc cac cca ggg ggt agt gcc cgc ttc cat tgt gcc 1329  
Thr Val Thr Ser Leu His Pro Gly Gly Ser Ala Arg Phe His Cys Ala  
370 375 380

act ggc tac cag ctg aag ggc gcc agg cat ctc acc tgt ctc aat gcc 1377  
Thr Gly Tyr Gln Leu Lys Gly Ala Arg His Leu Thr Cys Leu Asn Ala  
385 390 395 400

acc cag ccc ttc tgg gat tca aag gag ccc gtc tgc atc gct gct tgc 1425  
Thr Gln Pro Phe Trp Asp Ser Lys Glu Pro Val Cys Ile Ala Ala Cys  
405 410 415

ggc gga gtg atc cgc aat ggc acc acc ggc cgc atc gtc tct cca ggc 1473  
Gly Gly Val Ile Arg Asn Gly Thr Thr Gly Arg Ile Val Ser Pro Gly  
420 425 430

ttc ccg ggc aac tac agc aac aac ctc acc tgt cac tgg ctg ctt gag 1521  
Phe Pro Gly Asn Tyr Ser Asn Leu Thr Cys His Trp Leu Leu Glu  
435 440 445

gct cct gag ggc cag cgg cta cac ctg cac ttt gag aag gtt tcc ctg 1569  
Ala Pro Glu Gly Gln Arg Leu His Leu His Phe Glu Lys Val Ser Leu  
450 455 460

gca gag gat gat gac agg ctc atc att cgc aat ggg gac aac gtg gag 1617  
Ala Glu Asp Asp Asp Arg Leu Ile Ile Arg Asn Gly Asp Asn Val Glu  
465 470 475 480

gcc cca cca gtg gga aaa agc tcc ctg cag ctg ccc cgc ccc cgc ccc 1665  
Ala Pro Pro Val Gly Lys Ser Ser Leu Gln Leu Pro Arg Pro Arg Pro  
485 490 495

cgc ccc tac aac cgc att acc ata gag tca gcg ttt gac aat cca act 1713  
Arg Pro Tyr Asn Arg Ile Thr Ile Glu Ser Ala Phe Asp Asn Pro Thr  
500 505 510

tac gag act gga tct ctt tcc ttt gca gga gac gag aga ata 1755  
Tyr Glu Thr Gly Ser Leu Ser Phe Ala Gly Asp Glu Arg Ile  
515 520 525

tgaagtctcc atcttaggtgg gggcagtcta gggaaagtcaa ctcagacttg caccacagtc 1815

cagcagcaag gtccttgct tcctgtgtc cctccacctc ctgtatatac cacctaggag 1875

gagatgccac caagccctca agaagttgtg ccctccccg cctgcgtatgc ccaccatggc 1935

ctatttctt ggtgtattg cccacttggg gcccttgcat tggccatgt acagggggca 1995

tctacctgtg gggagaaca tagctggag cacaagcttc aacagccagc attccttgag 2055

cctccttcat ggccctggga ccagcctggg gaacacantt aggaggagc agggagttac 2115

cttgtttcac atgaccacca accattcc 2143

<210> 24

<211> 526

<212> PRT

<213> Homo sapiens

<223> n 2093 can be A, G, C, or T.

<400> 24

Met Arg Pro Val Ala Leu Leu Leu Leu Pro Ser Leu Leu Ala Leu Leu  
1 5 10 15

Ala His Gly Leu Ser Leu Glu Ala Pro Thr Val Gly Lys Gly Gln Ala  
20 25 30

Pro Gly Ile Glu Glu Thr Asp Gly Glu Leu Thr Ala Ala Pro Thr Pro  
35 40 45

Glu Gln Pro Glu Arg Gly Val His Phe Val Thr Thr Ala Pro Thr Leu  
50 55 60

Lys Leu Leu Asn His His Pro Leu Leu Glu Phe Leu Gln Glu Gly  
65 70 75 80

Leu Glu Lys Gly Asp Glu Glu Leu Arg Pro Ala Leu Pro Phe Gln Pro  
85 90 95

Asp Pro Pro Ala Pro Phe Thr Pro Ser Pro Leu Pro Arg Leu Ala Asn  
100 105 110

Gln Asp Ser Arg Pro Val Phe Thr Ser Pro Thr Pro Ala Met Ala Ala  
115 120 125

Val Pro Thr Gln Pro Gln Ser Lys Glu Gly Pro Trp Ser Pro Glu Ser  
130 135 140

Glu Ser Pro Met Leu Arg Ile Thr Ala Pro Leu Pro Pro Gly Pro Ser  
145 150 155 160

Met Ala Val Pro Thr Leu Gly Pro Gly Glu Ile Ala Ser Thr Thr Pro  
165 170 175

Pro Ser Arg Ala Trp Thr Pro Thr Gln Glu Gly Pro Gly Asp Met Gly  
180 185 190

Arg Pro Trp Val Ala Glu Val Val Ser Gln Gly Ala Gly Ile Gly Ile  
195 200 205

Gln Gly Thr Ile Thr Ser Ser Thr Ala Ser Gly Asp Asp Glu Glu Thr

210                  215                  220

Thr Thr Thr Thr Ile Ile Thr Thr Thr Ile Thr Val Gln Thr  
225                  230                  235                  240

Pro Gly Pro Cys Ser Trp Asn Phe Ser Gly Pro Glu Gly Ser Leu Asp  
245                  250                  255

Ser Pro Thr Asp Leu Ser Ser Pro Thr Asp Val Gly Leu Asp Cys Phe  
260                  265                  270

Phe Tyr Ile Ser Val Tyr Pro Gly Tyr Gly Val Glu Ile Lys Val Gln  
275                  280                  285

Asn Ile Ser Leu Arg Glu Gly Glu Thr Val Thr Val Glu Gly Leu Gly  
290                  295                  300

Gly Pro Asp Pro Leu Pro Leu Ala Asn Gln Ser Phe Leu Leu Arg Gly  
305                  310                  315                  320

Gln Val Ile Arg Ser Pro Thr His Gln Ala Ala Leu Arg Phe Gln Ser  
325                  330                  335

Leu Pro Pro Pro Ala Gly Pro Gly Thr Phe His Phe His Tyr Gln Ala  
340                  345                  350

Tyr Leu Leu Ser Cys His Phe Pro Arg Arg Pro Ala Tyr Gly Asp Val  
355                  360                  365

Thr Val Thr Ser Leu His Pro Gly Gly Ser Ala Arg Phe His Cys Ala  
370                  375                  380

Thr Gly Tyr Gln Leu Lys Gly Ala Arg His Leu Thr Cys Leu Asn Ala  
385                  390                  395                  400

Thr Gln Pro Phe Trp Asp Ser Lys Glu Pro Val Cys Ile Ala Ala Cys  
405                  410                  415

Gly Gly Val Ile Arg Asn Gly Thr Thr Gly Arg Ile Val Ser Pro Gly  
420                  425                  430

Phe Pro Gly Asn Tyr Ser Asn Asn Leu Thr Cys His Trp Leu Leu Glu  
435                  440                  445

Ala Pro Glu Gly Gln Arg Leu His Leu His Phe Glu Lys Val Ser Leu  
450                  455                  460

Ala Glu Asp Asp Asp Arg Leu Ile Ile Arg Asn Gly Asp Asn Val Glu  
465                  470                  475                  480

Ala Pro Pro Val Gly Lys Ser Ser Leu Gln Leu Pro Arg Pro Arg Pro  
485                  490                  495

Arg Pro Tyr Asn Arg Ile Thr Ile Glu Ser Ala Phe Asp Asn Pro Thr  
500                505                510

Tyr Glu Thr Gly Ser Leu Ser Phe Ala Gly Asp Glu Arg Ile  
515                520                525

<210> 25  
<211> 1482  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (178)..(960)

<400> 25  
ccaggcgctg gccgtggc tgattctgtc aggcgctggc ggccggcagcg gcgggtacgg 60  
ctgcggcccc gctccctcta cccggccgga cccggctctg ccccccgc cc aagccccac 120  
caagcccccc gccctccgc cgccgtccca gcccaggccg cggccgcaac cagcacc 177

atg cgc ccg gta gcc ctg ctg ctc ctg ccc tcg ctg gcg ctc ctg 225  
Met Arg Pro Val Ala Leu Leu Leu Leu Pro Ser Leu Leu Ala Leu Leu  
1                5                10                15

gct cac gga ctc tct tta gag gcc cca acc gtg ggg aaa gga caa gcc 273  
Ala His Gly Leu Ser Leu Glu Ala Pro Thr Val Gly Lys Gln Ala  
20                25                30

cca ggc atc gag gag aca gat ggc gag ctg aca gca gcc ccc aca cct 321  
Pro Gly Ile Glu Glu Thr Asp Gly Glu Leu Thr Ala Ala Pro Thr Pro  
35                40                45

gag cag cca gaa cga ggc gtc cac ttt gtc aca aca gcc ccc acc ttg 369  
Glu Gln Pro Glu Arg Gly Val His Phe Val Thr Thr Ala Pro Thr Leu  
50                55                60

aag ctg ctc aac cac cac ccg ctg ctt gag gaa ttc cta caa gag ggg 417  
Lys Leu Leu Asn His His Pro Leu Leu Glu Glu Phe Leu Gln Glu Gly  
65                70                75                80

ctg gaa aag gga gat gag gag ctg agg cca gca ctg ccc ttc cag cct 465  
Leu Glu Lys Gly Asp Glu Glu Leu Arg Pro Ala Leu Pro Phe Gln Pro  
85                90                95

gac cca cct gca ccc ttc acc cca agt ccc ctt ccc cgc ctg gcc aac 513  
Asp Pro Pro Ala Pro Phe Thr Pro Ser Pro Leu Pro Arg Leu Ala Asn  
100                105                110

cag gac agc cgc cct gtc ttt acc agc ccc act cca gcc atg gct gcg 561

Gln Asp Ser Arg Pro Val Phe Thr Ser Pro Thr Pro Ala Met Ala Ala  
115 120 125

gta ccc act cag ccc cag tcc aag gag gga ccc tgg agt ccg gag tca 609  
Val Pro Thr Gln Pro Gln Ser Lys Glu Gly Pro Trp Ser Pro Glu Ser  
130 135 140

gag tcc cct atg ctt cga atc aca gct ccc cta cct cca ggg ccc agc 657  
Glu Ser Pro Met Leu Arg Ile Thr Ala Pro Leu Pro Pro Gly Pro Ser  
145 150 155 160

atg gca gtg ccc acc cta ggc cca ggg gag ata gcc agc act aca ccc 705  
Met Ala Val Pro Thr Leu Gly Pro Gly Glu Ile Ala Ser Thr Thr Pro  
165 170 175

ccc agc aga gcc tgg aca cca acc caa gag ggt cct gga gac atg gga 753  
Pro Ser Arg Ala Trp Thr Pro Thr Gln Glu Gly Pro Gly Asp Met Gly  
180 185 190

agg ccg tgg gtt gca gag gtt gtg tcc cag ggc gca ggg atc ggg atc 801  
Arg Pro Trp Val Ala Glu Val Val Ser Gln Gly Ala Gly Ile Gly Ile  
195 200 205

cag ggg acc atc acc tcc tcc aca gct tca gga gat gat gag gag acc 849  
Gln Gly Thr Ile Thr Ser Ser Thr Ala Ser Gly Asp Asp Glu Glu Thr  
210 215 220

acc act acc acc atc atc acc acc acc atc acc aca gtc cag aca 897  
Thr Thr Thr Thr Ile Ile Thr Thr Ile Thr Thr Val Gln Thr  
225 230 235 240

cca ggt cag cta cct gct ggc ttg cag atg tgg aaa ttg gga ttg ggg 945  
Pro Gly Gln Leu Pro Ala Gly Leu Gln Met Trp Lys Trp Gly Trp Gly  
245 250 255

agg ctg cgg ggc ccc taaaagcctg tctctgacac tgtgccagcc tgccctgcc 1000  
Arg Leu Arg Gly Pro  
260

tttggcacca agggccagcc tgcaggaggc atgttagattg gacccagata gacctgagct 1060

caaatcctga ttcttcagcc aagtacagtg gctcatgcct gtaatcccgactttggga 1120

ggcagaggcc agtggatcat ctgaggtcag gagttcaaga ccctcctggc caacatggcg 1180

aaacaccatc tctactaaaa atacaaaaaat gagccgggca tggtggtggg cacctgtaat 1240

cccagctact cgggaggctg aggcaggaga atcactcaa cctggaggc agaggttgca 1300

gtgagctgag attgcaccaat tgcactccag cctggcaac agagcgagac tctgtctcaa 1360

aaaagaaaaaa atcttgattc ttccaactat aacatgaccc taggaattct atttaacatc 1420

tcatctctga gcctcatctg taaaatggca ataagaaaaat aaacttctgg ctagaaaaaaaa 1480

aa 1482

<210> 26

<211> 261

<212> PRT

<213> Homo sapiens

<400> 26

Met Arg Pro Val Ala Leu Leu Leu Leu Pro Ser Leu Leu Ala Leu Leu  
1 5 10 15

Ala His Gly Leu Ser Leu Glu Ala Pro Thr Val Gly Lys Gly Gln Ala  
20 25 30

Pro Gly Ile Glu Glu Thr Asp Gly Glu Leu Thr Ala Ala Pro Thr Pro  
35 40 45

Glu Gln Pro Glu Arg Gly Val His Phe Val Thr Thr Ala Pro Thr Leu  
50 55 60

Lys Leu Leu Asn His His Pro Leu Leu Glu Glu Phe Leu Gln Glu Gly  
65 70 75 80

Leu Glu Lys Gly Asp Glu Glu Leu Arg Pro Ala Leu Pro Phe Gln Pro  
85 90 95

Asp Pro Pro Ala Pro Phe Thr Pro Ser Pro Leu Pro Arg Leu Ala Asn  
100 105 110

Gln Asp Ser Arg Pro Val Phe Thr Ser Pro Thr Pro Ala Met Ala Ala  
115 120 125

Val Pro Thr Gln Pro Gln Ser Lys Glu Gly Pro Trp Ser Pro Glu Ser  
130 135 140

Glu Ser Pro Met Leu Arg Ile Thr Ala Pro Leu Pro Pro Gly Pro Ser  
145 150 155 160

Met Ala Val Pro Thr Leu Gly Pro Gly Glu Ile Ala Ser Thr Thr Pro  
165 170 175

Pro Ser Arg Ala Trp Thr Pro Thr Gln Glu Gly Pro Gly Asp Met Gly  
180 185 190

Arg Pro Trp Val Ala Glu Val Val Ser Gln Gly Ala Gly Ile Gly Ile  
195 200 205

Gln Gly Thr Ile Thr Ser Ser Thr Ala Ser Gly Asp Asp Glu Glu Thr  
210 215 220

Thr Thr Thr Thr Ile Ile Thr Thr Thr Ile Thr Val Gln Thr  
225            230            235            240

Pro Gly Gln Leu Pro Ala Gly Leu Gln Met Trp Lys Trp Gly Trp Gly  
245            250            255

Arg Leu Arg Gly Pro  
260

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<212> DNA  
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<222> (120)..(2639)

<220>  
<223> n 3325 can be A, G, C, or T.

<400> 27  
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tcggcgccggc cttccctcc tcctccgtct cctccatct ctctccatct gctgtggtt 119

atg gcc tgt cgc tgg agc aca aaa gag tct ccg cggtt agg tct gcg 167  
Met Ala Cys Arg Trp Ser Thr Lys Glu Ser Pro Arg Trp Arg Ser Ala  
1            5            10            15

ttg ctc ttg ctt ttc ctc gct ggg gtg tac gct tgt gga gag act cca 215  
Leu Leu Leu Phe Leu Ala Gly Val Tyr Ala Cys Gly Glu Thr Pro  
20            25            30

gag caa ata cga gca cca agt ggc ata atc aca agc cca ggc tgg cct 263  
Glu Gln Ile Arg Ala Pro Ser Gly Ile Ile Thr Ser Pro Gly Trp Pro  
35            40            45

tct gaa tat cct gca aaa atc aac tgt agc tgg ttc ata agg gca aac 311  
Ser Glu Tyr Pro Ala Lys Ile Asn Cys Ser Trp Phe Ile Arg Ala Asn  
50            55            60

cca ggc gaa atc att act ata agt ttt cag gat ttt gat att caa gga 359  
Pro Gly Glu Ile Ile Thr Ile Ser Phe Gln Asp Phe Asp Ile Gln Gly  
65            70            75            80

tcc aga agg tgc aat ttg gac tgg ttg aca ata gaa aca tac aag aat 407  
Ser Arg Arg Cys Asn Leu Asp Trp Leu Thr Ile Glu Thr Tyr Lys Asn  
85            90            95

att gaa agt tac aga gct tgt ggt tcc aca att cca cct ccg tat atc 455

Ile Glu Ser Tyr Arg Ala Cys Gly Ser Thr Ile Pro Pro Pro Tyr Ile  
100                105                110

tct tca caa gac cac atc tgg att agg ttt cat tcg gat gac aac atc 503  
Ser Ser Gln Asp His Ile Trp Ile Arg Phe His Ser Asp Asp Asn Ile  
115                120                125

tct aga aag ggt ttc aga ctg gca tat ttt tca ggg aaa tct gag gaa 551  
Ser Arg Lys Gly Phe Arg Leu Ala Tyr Phe Ser Gly Lys Ser Glu Glu  
130                135                140

cca aat tgt gct tgt gat cag ttt cgt tgt ggt aat gga aag tgt ata 599  
Pro Asn Cys Ala Cys Asp Gln Phe Arg Cys Gly Asn Gly Lys Cys Ile  
145                150                155                160

cca gaa gcc tgg aaa tgc aat aac atg gat gaa tgt gga gat agt tcc 647  
Pro Glu Ala Trp Lys Cys Asn Asn Met Asp Glu Cys Gly Asp Ser Ser  
165                170                175

gat gaa gag atc tgt gcc aaa gaa gca aat cct cca act gct gct gct 695  
Asp Glu Glu Ile Cys Ala Lys Glu Ala Asn Pro Pro Thr Ala Ala Ala  
180                185                190

ttt caa ccc tgt gct tac aac cag ttc cag tgt tta tcc cgt tt acc 743  
Phe Gln Pro Cys Ala Tyr Asn Gln Phe Gln Cys Leu Ser Arg Phe Thr  
195                200                205

aaa gtt tac act tgc ctc ccc gaa tct tta aaa tgt gat ggg aac att 791  
Lys Val Tyr Thr Cys Leu Pro Glu Ser Leu Lys Cys Asp Gly Asn Ile  
210                215                220

gac tgc ctt gac cta gga gat gag ata gac tgt gat gtg cca aca tgt 839  
Asp Cys Leu Asp Leu Gly Asp Glu Ile Asp Cys Asp Val Pro Thr Cys  
225                230                235                240

ggg caa tgg cta aaa tat ttt tat ggt act ttt aat tct ccc aat tat 887  
Gly Gln Trp Leu Lys Tyr Phe Tyr Gly Thr Phe Asn Ser Pro Asn Tyr  
245                250                255

cca gac ttt tat cct cct gga agc aat tgc acc tgg tta ata gac act 935  
Pro Asp Phe Tyr Pro Pro Gly Ser Asn Cys Thr Trp Leu Ile Asp Thr  
260                265                270

ggt gat cac cgt aaa gtc att tta cgc ttc act gac ttt aaa ctt gat 983  
Gly Asp His Arg Lys Val Ile Leu Arg Phe Thr Asp Phe Lys Leu Asp  
275                280                285

ggt act ggt tat ggt gat tat gtc aaa ata tat gat gga tta gag gag 1031  
Gly Thr Gly Tyr Gly Asp Tyr Val Lys Ile Tyr Asp Gly Leu Glu Glu  
290                295                300

aat cca cac aag ctt ttg cgt gtg aca gct ttt gat tct cat gca 1079  
Asn Pro His Lys Leu Leu Arg Val Leu Thr Ala Phe Asp Ser His Ala

305            310            315            320  
cct ctt aca gtt gtt tct tct gga cag ata agg gta cat ttt tgt 1127  
Pro Leu Thr Val Val Ser Ser Ser Gly Gln Ile Arg Val His Phe Cys  
325            330            335  
  
gct gat aaa gtg aat gct gca agg gga ttt aat gct act tac caa gta 1175  
Ala Asp Lys Val Asn Ala Ala Arg Gly Phe Asn Ala Thr Tyr Gln Val  
340            345            350  
  
gat ggg ttc tgt ttg cca tgg gaa ata ccc tgt gga ggt aac tgg ggg 1223  
Asp Gly Phe Cys Leu Pro Trp Glu Ile Pro Cys Gly Gly Asn Trp Gly  
355            360            365  
  
tgt tat act gag cag cag cgt tgt gat ggg tat tgg cat tgc cca aat 1271  
Cys Tyr Thr Glu Gln Gln Arg Cys Asp Gly Tyr Trp His Cys Pro Asn  
370            375            380  
  
gga agg gat gaa acc aat tgt acc atg tgc cag aag gaa gaa ttt cca 1319  
Gly Arg Asp Glu Thr Asn Cys Thr Met Cys Gln Lys Glu Glu Phe Pro  
385            390            395            400  
  
tgt tcc cga aat ggt gtc tgt tat cct cgt tct gat cgc tgc aac tac 1367  
Cys Ser Arg Asn Gly Val Cys Tyr Pro Arg Ser Asp Arg Cys Asn Tyr  
405            410            415  
  
cag aat cat tgc cca aat ggc tca gat gaa aaa aac tgc ttt ttt tgc 1415  
Gln Asn His Cys Pro Asn Gly Ser Asp Glu Lys Asn Cys Phe Phe Cys  
420            425            430  
  
caa cca gga aat ttc cat tgt aaa aac aat cgt tgt gtg ttt gaa agt 1463  
Gln Pro Gly Asn Phe His Cys Lys Asn Asn Arg Cys Val Phe Glu Ser  
435            440            445  
  
tgg gtg tgt gat tct caa gat gac tgt ggt gat ggc agc gat gaa gaa 1511  
Trp Val Cys Asp Ser Gln Asp Asp Cys Gly Asp Gly Ser Asp Glu Glu  
450            455            460  
  
aat tgc cca gta atc gtg cct aca aga gtc atc act gct gcc gtc ata 1559  
Asn Cys Pro Val Ile Val Pro Thr Arg Val Ile Thr Ala Ala Val Ile  
465            470            475            480  
  
ggg agc ctc atc tgt ggc ctg tta ctc gtc ata gca ttg gga tgt act 1607  
Gly Ser Leu Ile Cys Gly Leu Leu Leu Val Ile Ala Leu Gly Cys Thr  
485            490            495  
  
tgt aag ctt tat tct ctg aga atg ttt gaa aga aga tca ttt gaa aca 1655  
Cys Lys Leu Tyr Ser Leu Arg Met Phe Glu Arg Arg Ser Phe Glu Thr  
500            505            510  
  
cag ttg tca aga gtg gaa gca gaa ttg tta aga aga gaa gct cct ccc 1703  
Gln Leu Ser Arg Val Glu Ala Glu Leu Leu Arg Arg Glu Ala Pro Pro  
515            520            525

tcg tat gga caa ttg att gct cag ggt tta att cca cca gtt gaa gat 1751  
Ser Tyr Gly Gln Leu Ile Ala Gln Gly Leu Ile Pro Pro Val Glu Asp  
530 535 540

ttt cct gtt tgt tca cct aat cag gct tct gtt ttg gaa aat ctg agg 1799  
Phe Pro Val Cys Ser Pro Asn Gln Ala Ser Val Leu Glu Asn Leu Arg  
545 550 555 560

cta gcg gta cga tct cag ctt gga ttt act tca gtc agg ctt cct atg 1847  
Leu Ala Val Arg Ser Gln Leu Gly Phe Thr Ser Val Arg Leu Pro Met  
565 570 575

gca ggc aga tca agc aac att tgg aac cgt att ttt aat ttt gca aga 1895  
Ala Gly Arg Ser Ser Asn Ile Trp Asn Arg Ile Phe Asn Phe Ala Arg  
580 585 590

tca cgt cat tct ggg tca ttg gct ttc tca gca gat gga gat gag 1943  
Ser Arg His Ser Gly Ser Leu Ala Leu Val Ser Ala Asp Gly Asp Glu  
595 600 605

gtt gtc cct agt cag agt acc agt aga gaa cct gag aga aat cat act 1991  
Val Val Pro Ser Gln Ser Thr Ser Arg Glu Pro Glu Arg Asn His Thr  
610 615 620

cac aga agt ttg ttt tcc gtg gag tct gat gat aca gac aca gaa aat 2039  
His Arg Ser Leu Phe Ser Val Glu Ser Asp Asp Thr Asp Thr Glu Asn  
625 630 635 640

gag aga aga gat atg gca gga gca tct ggt ggg gtt gca gct cct ttg 2087  
Glu Arg Arg Asp Met Ala Gly Ala Ser Gly Gly Val Ala Ala Pro Leu  
645 650 655

cct caa aaa gtc cct ccc aca acg gca gta gaa gcg aca gta gga gca 2135  
Pro Gln Lys Val Pro Pro Thr Thr Ala Val Glu Ala Thr Val Gly Ala  
660 665 670

tgt gca agt tcc tca act cag agt acc cga ggt ggt cat gca gat aat 2183  
Cys Ala Ser Ser Ser Thr Gln Ser Thr Arg Gly Gly His Ala Asp Asn  
675 680 685

gga agg gat gtg aca agt gtg gaa ccc cca agt gtg agt cca gca cgt 2231  
Gly Arg Asp Val Thr Ser Val Glu Pro Pro Ser Val Ser Pro Ala Arg  
690 695 700

cac cag ctt aca agt gca ctc agt cgt atg act cag ggg cta cgc tgg 2279  
His Gln Leu Thr Ser Ala Leu Ser Arg Met Thr Gln Gly Leu Arg Trp  
705 710 715 720

gta cgt ttt aca tta gga cga tca agt tcc cta agt cag aac cag agt 2327  
Val Arg Phe Thr Leu Gly Arg Ser Ser Ser Leu Ser Gln Asn Gln Ser  
725 730 735

cct ttg aga caa ctt gat aat ggg gta agt gga aga gaa gat gat gat 2375  
Pro Leu Arg Gln Leu Asp Asn Gly Val Ser Gly Arg Glu Asp Asp Asp  
740 745 750

gat gtt gaa atg cta att cca att tct gat gga tct tca gac ttt gat 2423  
Asp Val Glu Met Leu Ile Pro Ile Ser Asp Gly Ser Ser Asp Phe Asp  
755 760 765

gtg aat gac tgc tcc aga cct ctt gat ctt gcc tca gat caa gga 2471  
Val Asn Asp Cys Ser Arg Pro Leu Leu Asp Leu Ala Ser Asp Gln Gly  
770 775 780

caa ggg ctt aga caa cca tat aat gca aca aat cct gga gta agg cca 2519  
Gln Gly Leu Arg Gln Pro Tyr Asn Ala Thr Asn Pro Gly Val Arg Pro  
785 790 795 800

agt aat cga gat ggc ccc tgt gag cgc tgt ggt att gtc cac act gcc 2567  
Ser Asn Arg Asp Gly Pro Cys Glu Arg Cys Gly Ile Val His Thr Ala  
805 810 815

cag ata cca gac act tgc tta gaa gta aca ctg aaa aac gaa acg agt 2615  
Gln Ile Pro Asp Thr Cys Leu Glu Val Thr Leu Lys Asn Glu Thr Ser  
820 825 830

gat gat gag gct ttg tta ctt tgt tagtgtacgaa tcacataagg gagattgtat 2669  
Asp Asp Glu Ala Leu Leu Leu Cys  
835 840

acaagttgga gcaatatcca ttattatttt tgtaacttta cagttaaact agtttagtt 2729  
taaaaagaaa aaatgcaggg tgatttctta ttattatatg tttagcctgca tggtaaatt 2789

cgacaaacttg taactctatg aacttagagt ttactatttt agcagctaaa aatgcatcac 2849

atattgcata ttgtcaata atggccctt catttgttgc tgattgtttt catcctgata 2909

ctgttagttca ctgtagaaat gtggctgctg aaactcattt gattgtcattt tttatctatc 2969

ctatgttaaa tggtttggttt ttacaaaata atacctattt ttaattgaaa cgtttatgct 3029

tttgcacacatcttgcata acttaatata gctagatgtt aagggttgcata atgtacaaaa 3089

aaaaaaaaaac ttataactca cctgcgtttt catttgttgc acatgttgcattt attattggat 3149

atcattatca tatgaacttg tcagttggaa acaaactgtc taaaattttt tctcttacgt 3209

ttaacataca atcatgtgag atttaggcag agttcgataa attactggca aaaacaaaaac 3269

tcatttataaa agattttcta atgttgactt taatactcta acatggtaca aaccanatgg 3329

taaaatc 3336

<210> 28

<211> 840

<212> PRT

<213> Homo sapiens

<223> n 3325 can be A, G, C, or T.

<400> 28

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Leu Leu Leu Leu Phe Leu Ala Gly Val Tyr Ala Cys Gly Glu Thr Pro  
20 25 30

Glu Gln Ile Arg Ala Pro Ser Gly Ile Ile Thr Ser Pro Gly Trp Pro  
35 40 45

Ser Glu Tyr Pro Ala Lys Ile Asn Cys Ser Trp Phe Ile Arg Ala Asn  
50 55 60

Pro Gly Glu Ile Ile Thr Ile Ser Phe Gln Asp Phe Asp Ile Gln Gly  
65 70 75 80

Ser Arg Arg Cys Asn Leu Asp Trp Leu Thr Ile Glu Thr Tyr Lys Asn  
85 90 95

Ile Glu Ser Tyr Arg Ala Cys Gly Ser Thr Ile Pro Pro Pro Tyr Ile  
100 105 110

Ser Ser Gln Asp His Ile Trp Ile Arg Phe His Ser Asp Asp Asn Ile  
115 120 125

Ser Arg Lys Gly Phe Arg Leu Ala Tyr Phe Ser Gly Ser Glu Glu  
130 135 140

Pro Asn Cys Ala Cys Asp Gln Phe Arg Cys Gly Asn Gly Lys Cys Ile  
145 150 155 160

Pro Glu Ala Trp Lys Cys Asn Asn Met Asp Glu Cys Gly Asp Ser Ser  
165 170 175

Asp Glu Glu Ile Cys Ala Lys Glu Ala Asn Pro Pro Thr Ala Ala Ala  
180 185 190

Phe Gln Pro Cys Ala Tyr Asn Gln Phe Gln Cys Leu Ser Arg Phe Thr  
195 200 205

Lys Val Tyr Thr Cys Leu Pro Glu Ser Leu Lys Cys Asp Gly Asn Ile  
210 215 220

Asp Cys Leu Asp Leu Gly Asp Glu Ile Asp Cys Asp Val Pro Thr Cys  
225 230 235 240

Gly Gln Trp Leu Lys Tyr Phe Tyr Gly Thr Phe Asn Ser Pro Asn Tyr

245 250 255

Pro Asp Phe Tyr Pro Pro Gly Ser Asn Cys Thr Trp Leu Ile Asp Thr  
260 265 270

Gly Asp His Arg Lys Val Ile Leu Arg Phe Thr Asp Phe Lys Leu Asp  
275 280 285

Gly Thr Gly Tyr Gly Asp Tyr Val Lys Ile Tyr Asp Gly Leu Glu Glu  
290 295 300

Asn Pro His Lys Leu Leu Arg Val Leu Thr Ala Phe Asp Ser His Ala  
305 310 315 320

Pro Leu Thr Val Val Ser Ser Gly Gln Ile Arg Val His Phe Cys  
325 330 335

Ala Asp Lys Val Asn Ala Ala Arg Gly Phe Asn Ala Thr Tyr Gln Val  
340 345 350

Asp Gly Phe Cys Leu Pro Trp Glu Ile Pro Cys Gly Gly Asn Trp Gly  
355 360 365

Cys Tyr Thr Glu Gln Gln Arg Cys Asp Gly Tyr Trp His Cys Pro Asn  
370 375 380

Gly Arg Asp Glu Thr Asn Cys Thr Met Cys Gln Lys Glu Glu Phe Pro  
385 390 395 400

Cys Ser Arg Asn Gly Val Cys Tyr Pro Arg Ser Asp Arg Cys Asn Tyr  
405 410 415

Gln Asn His Cys Pro Asn Gly Ser Asp Glu Lys Asn Cys Phe Phe Cys  
420 425 430

Gln Pro Gly Asn Phe His Cys Lys Asn Asn Arg Cys Val Phe Glu Ser  
435 440 445

Trp Val Cys Asp Ser Gln Asp Asp Cys Gly Asp Gly Ser Asp Glu Glu  
450 455 460

Asn Cys Pro Val Ile Val Pro Thr Arg Val Ile Thr Ala Ala Val Ile  
465 470 475 480

Gly Ser Leu Ile Cys Gly Leu Leu Leu Val Ile Ala Leu Gly Cys Thr  
485 490 495

Cys Lys Leu Tyr Ser Leu Arg Met Phe Glu Arg Arg Ser Phe Glu Thr  
500 505 510

Gln Leu Ser Arg Val Glu Ala Glu Leu Leu Arg Arg Glu Ala Pro Pro  
515 520 525

Ser Tyr Gly Gln Leu Ile Ala Gln Gly Leu Ile Pro Pro Val Glu Asp  
530                535                540

Phe Pro Val Cys Ser Pro Asn Gln Ala Ser Val Leu Glu Asn Leu Arg  
545                550                555                560

Leu Ala Val Arg Ser Gln Leu Gly Phe Thr Ser Val Arg Leu Pro Met  
565                570                575

Ala Gly Arg Ser Ser Asn Ile Trp Asn Arg Ile Phe Asn Phe Ala Arg  
580                585                590

Ser Arg His Ser Gly Ser Leu Ala Leu Val Ser Ala Asp Gly Asp Glu  
595                600                605

Val Val Pro Ser Gln Ser Thr Ser Arg Glu Pro Glu Arg Asn His Thr  
610                615                620

His Arg Ser Leu Phe Ser Val Glu Ser Asp Asp Thr Asp Thr Glu Asn  
625                630                635                640

Glu Arg Arg Asp Met Ala Gly Ala Ser Gly Gly Val Ala Ala Pro Leu  
645                650                655

Pro Gln Lys Val Pro Pro Thr Thr Ala Val Glu Ala Thr Val Gly Ala  
660                665                670

Cys Ala Ser Ser Ser Thr Gln Ser Thr Arg Gly Gly His Ala Asp Asn  
675                680                685

Gly Arg Asp Val Thr Ser Val Glu Pro Pro Ser Val Ser Pro Ala Arg  
690                695                700

His Gln Leu Thr Ser Ala Leu Ser Arg Met Thr Gln Gly Leu Arg Trp  
705                710                715                720

Val Arg Phe Thr Leu Gly Arg Ser Ser Ser Leu Ser Gln Asn Gln Ser  
725                730                735

Pro Leu Arg Gln Leu Asp Asn Gly Val Ser Gly Arg Glu Asp Asp Asp  
740                745                750

Asp Val Glu Met Leu Ile Pro Ile Ser Asp Gly Ser Ser Asp Phe Asp  
755                760                765

Val Asn Asp Cys Ser Arg Pro Leu Leu Asp Leu Ala Ser Asp Gln Gly  
770                775                780

Gln Gly Leu Arg Gln Pro Tyr Asn Ala Thr Asn Pro Gly Val Arg Pro  
785                790                795                800

Ser Asn Arg Asp Gly Pro Cys Glu Arg Cys Gly Ile Val His Thr Ala  
805                810                815

Gln Ile Pro Asp Thr Cys Leu Glu Val Thr Leu Lys Asn Glu Thr Ser  
820                825                830

Asp Asp Glu Ala Leu Leu Leu Cys  
835                840

<210> 29  
<211> 1498  
<212> DNA  
<213> Homo sapiens

<220>  
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<222> (120)..(1466)

<400> 29  
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tcccagctcc tcccccctcc tccctccgtct cctccctctt ctctccatct gctgtggtt 119

atg gcc tgt cgc tgg agc aca aaa gag tct ccg cgg tgg agg tct gcg 167  
Met Ala Cys Arg Trp Ser Thr Lys Glu Ser Pro Arg Trp Arg Ser Ala  
1                5                10                15

ttg ctc ttg ctt ttc ctc gct ggg gtg tac gga aat ggt gct ctt gca 215  
Leu Leu Leu Phe Leu Ala Gly Val Tyr Gly Asn Gly Ala Leu Ala  
20                25                30

gaa cat tct gaa aat gtg cat att tca gga gtg tca act gct tgt gga 263  
Glu His Ser Glu Asn Val His Ile Ser Gly Val Ser Thr Ala Cys Gly  
35                40                45

gag act cca gag caa ata cga gca cca agt ggc ata atc aca agc cca 311  
Glu Thr Pro Glu Gln Ile Arg Ala Pro Ser Gly Ile Ile Thr Ser Pro  
50                55                60

ggc tgg cct tct gaa tat cct gca aaa atc aac tgt agc tgg ttc ata 359  
Gly Trp Pro Ser Glu Tyr Pro Ala Lys Ile Asn Cys Ser Trp Phe Ile  
65                70                75                80

agg gca aac cca ggc gaa atc att act ata agt ttt cag gat ttt gat 407  
Arg Ala Asn Pro Gly Glu Ile Ile Thr Ile Ser Phe Gln Asp Phe Asp  
85                90                95

att caa gga tcc aga agg tgc aat ttg gac tgg ttg aca ata gaa aca 455  
Ile Gln Gly Ser Arg Arg Cys Asn Leu Asp Trp Leu Thr Ile Glu Thr  
100                105                110

tac aag aat att gaa agt tac aga gct tgt ggt tcc aca att cca cct 503  
Tyr Lys Asn Ile Glu Ser Tyr Arg Ala Cys Gly Ser Thr Ile Pro Pro

115

120

125

ccg tat atc tct tca caa gac cac atc tgg att agg ttt cat tcg gat 551  
Pro Tyr Ile Ser Ser Gln Asp His Ile Trp Ile Arg Phe His Ser Asp  
130 135 140

gac aac atc tct aga aag ggt ttc aga ctg gca tat ttt tca ggg aaa 599  
Asp Asn Ile Ser Arg Lys Gly Phe Arg Leu Ala Tyr Phe Ser Gly Lys  
145 150 155 160

tct gag gaa cca aat tgt gct tgt gat cag ttt cgt tgt ggt aat gga 647  
Ser Glu Glu Pro Asn Cys Ala Cys Asp Gln Phe Arg Cys Gly Asn Gly  
165 170 175

aag tgt ata cca gaa gcc tgg aaa tgt aat aac atg gat gaa tgt gga 695  
Lys Cys Ile Pro Glu Ala Trp Lys Cys Asn Asn Met Asp Glu Cys Gly  
180 185 190

gat agt tcc gat gaa gag atc tgt gcc aaa gaa gca aat cct cca act 743  
Asp Ser Ser Asp Glu Glu Ile Cys Ala Lys Glu Ala Asn Pro Pro Thr  
195 200 205

gct gct gct ttt caa ccc tgt gct tac aac cag ttc cag tgt tta tcc 791  
Ala Ala Ala Phe Gin Pro Cys Ala Tyr Asn Gln Phe Glu Cys Leu Ser  
210 215 220

cgt ttt acc aaa gtt tac act tgc ctc ccc gaa tct tta aaa tgt gat 839  
Arg Phe Thr Lys Val Tyr Thr Cys Leu Pro Glu Ser Leu Lys Cys Asp  
225 230 235 240

ggg aac att gac tgc ctt gac cta gga gat gag ata gac tgt gat gtg 887  
Gly Asn Ile Asp Cys Leu Asp Leu Gly Asp Glu Ile Asp Cys Asp Val  
245 250 255

cca aca tgt ggg caa tgg cta aaa tat ttt tat ggt act ttt aat tct 935  
Pro Thr Cys Gly Gln Trp Leu Lys Tyr Phe Tyr Gly Thr Phe Asn Ser  
260 265 270

ccc aat tat cca gac ttt tat cct cct gga agc aat tgc acc tgg tta 983  
Pro Asn Tyr Pro Asp Phe Tyr Pro Pro Gly Ser Asn Cys Thr Trp Leu  
275 280 285

ata gac act ggt gat cac cgt aaa gtc att tta cgc ttc act gac ttt 1031  
Ile Asp Thr Gly Asp His Arg Lys Val Ile Leu Arg Phe Thr Asp Phe  
290 295 300

aaa ctt gat ggt act ggt tat ggt gat tat gtc aaa ata tat gat gga 1079  
Lys Leu Asp Gly Thr Gly Tyr Asp Tyr Val Lys Ile Tyr Asp Gly  
305 310 315 320

tta gag gag aat cca cac aag ctt ttg cgt gtg ttg aca gct ttt gat 1127  
Leu Glu Glu Asn Pro His Lys Leu Leu Arg Val Leu Thr Ala Phe Asp  
325 330 335

tct cat gca cct ctt aca gtt gtt tct tct gga cag ata agg gta 1175  
Ser His Ala Pro Leu Thr Val Val Ser Ser Ser Gly Gln Ile Arg Val  
340 345 350

cat ttt tgt gct gat aaa gtg aat gct gca agg gga ttt aat gct act 1223  
His Phe Cys Ala Asp Lys Val Asn Ala Ala Arg Gly Phe Asn Ala Thr  
355 360 365

tac caa gta gat ggg ttc tgt ttg cca tgg gaa ata ccc tgt gga ggt 1271  
Tyr Gln Val Asp Gly Phe Cys Leu Pro Trp Glu Ile Pro Cys Gly Gly  
370 375 380

aac tgg ggg tgt tat act gag cag cgt cgt gat ggg tat tgg cat 1319  
Asn Trp Gly Cys Tyr Thr Glu Gln Gln Arg Arg Asp Gly Tyr Trp His  
385 390 395 400

tgc cca aat gga agg gat gaa acc aat tgt acc atg tgc cag aag gaa 1367  
Cys Pro Asn Gly Arg Asp Glu Thr Asn Cys Thr Met Cys Gln Lys Glu  
405 410 415

gaa ttt cca tgt tcc cga aat ggt gtc tgt tat cct cgt tct gat cgc 1415  
Glu Phe Pro Cys Ser Arg Asn Gly Val Cys Tyr Pro Arg Ser Asp Arg  
420 425 430

tgc aac tac cag aat cat tgc cca aat ggc aaa cag aac cca tct act 1463  
Cys Asn Tyr Gln Asn His Cys Pro Asn Gly Lys Gln Asn Pro Ser Thr  
435 440 445

tgg taatccccct tgccatcattc ac 1498  
Trp

<210> 30  
<211> 449  
<212> PRT  
<213> Homo sapiens

<400> 30  
Met Ala Cys Arg Trp Ser Thr Lys Glu Ser Pro Arg Trp Arg Ser Ala  
1 5 10 15

Leu Leu Leu Leu Phe Leu Ala Gly Val Tyr Gly Asn Gly Ala Leu Ala  
20 25 30

Glu His Ser Glu Asn Val His Ile Ser Gly Val Ser Thr Ala Cys Gly  
35 40 45

Glu Thr Pro Glu Gln Ile Arg Ala Pro Ser Gly Ile Ile Thr Ser Pro  
50 55 60

Gly Trp Pro Ser Glu Tyr Pro Ala Lys Ile Asn Cys Ser Trp Phe Ile  
65 70 75 80

Arg Ala Asn Pro Gly Glu Ile Ile Thr Ile Ser Phe Gln Asp Phe Asp  
85 90 95

Ile Gln Gly Ser Arg Arg Cys Asn Leu Asp Trp Leu Thr Ile Glu Thr  
100 105 110

Tyr Lys Asn Ile Glu Ser Tyr Arg Ala Cys Gly Ser Thr Ile Pro Pro  
115 120 125

Pro Tyr Ile Ser Ser Gln Asp His Ile Trp Ile Arg Phe His Ser Asp  
130 135 140

Asp Asn Ile Ser Arg Lys Gly Phe Arg Leu Ala Tyr Phe Ser Gly Lys  
145 150 155 160

Ser Glu Glu Pro Asn Cys Ala Cys Asp Gln Phe Arg Cys Gly Asn Gly  
165 170 175

Lys Cys Ile Pro Glu Ala Trp Lys Cys Asn Asn Met Asp Glu Cys Gly  
180 185 190

Asp Ser Ser Asp Glu Glu Ile Cys Ala Lys Glu Ala Asn Pro Pro Thr  
195 200 205

Ala Ala Ala Phe Gln Pro Cys Ala Tyr Asn Gln Phe Gln Cys Leu Ser  
210 215 220

Arg Phe Thr Lys Val Tyr Thr Cys Leu Pro Glu Ser Leu Lys Cys Asp  
225 230 235 240

Gly Asn Ile Asp Cys Leu Asp Leu Gly Asp Glu Ile Asp Cys Asp Val  
245 250 255

Pro Thr Cys Gly Gln Trp Leu Lys Tyr Phe Tyr Gly Thr Phe Asn Ser  
260 265 270

Pro Asn Tyr Pro Asp Phe Tyr Pro Pro Gly Ser Asn Cys Thr Trp Leu  
275 280 285

Ile Asp Thr Gly Asp His Arg Lys Val Ile Leu Arg Phe Thr Asp Phe  
290 295 300

Lys Leu Asp Gly Thr Gly Tyr Gly Asp Tyr Val Lys Ile Tyr Asp Gly  
305 310 315 320

Leu Glu Glu Asn Pro His Lys Leu Leu Arg Val Leu Thr Ala Phe Asp  
325 330 335

Ser His Ala Pro Leu Thr Val Val Ser Ser Gly Gln Ile Arg Val  
340 345 350

His Phe Cys Ala Asp Lys Val Asn Ala Ala Arg Gly Phe Asn Ala Thr

355 360 365

Tyr Gln Val Asp Gly Phe Cys Leu Pro Trp Glu Ile Pro Cys Gly Gly

370 375 380

Asn Trp Gly Cys Tyr Thr Glu Gln Gln Arg Arg Asp Gly Tyr Trp His

385 390 395 400

Cys Pro Asn Gly Arg Asp Glu Thr Asn Cys Thr Met Cys Gln Lys Glu

405 410 415

Glu Phe Pro Cys Ser Arg Asn Gly Val Cys Tyr Pro Arg Ser Asp Arg

420 425 430

Cys Asn Tyr Gln Asn His Cys Pro Asn Gly Lys Gln Asn Pro Ser Thr

435 440 445

Trp

<210> 31

<211> 691

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (203)..(571)

<400> 31

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ctccggggagc ggcagcagta gccccggcgcc cgaggggctgg gggttcctcg agactctcag 120

agggggcgcct cccatcgccg cccaccaccc caaccgttcc ctgcgcgcgc actgcgcgtgc 180

gccccaggac ccgcgtgcaca ac atg gat ttt ctc ctg gcg ctg gtg ctg gta 232

Met Asp Phe Leu Leu Ala Leu Val Leu Val

1 5 10

tcc tcg ctc tac ctg cag gcg gcc gag tac gac ggg agg tgg ccc 280

Ser Ser Leu Tyr Leu Gln Ala Ala Ala Glu Tyr Asp Gly Arg Trp Pro

15 20 25

agg caa ata gtg tca tcg att ggc cta tgt cgt tat ggt ggg agg att 328

Arg Gln Ile Val Ser Ser Ile Gly Leu Cys Arg Tyr Gly Gly Arg Ile

30 35 40

gac tgc tgc tgg ggc tgg gct cgc cag tct tgg gga cag tgt cag cct 376

Asp Cys Cys Trp Gly Trp Ala Arg Gln Ser Trp Gly Gln Cys Gln Pro

45 50 55

ttc tac gtc tta agg cag aga ata gcc agg ata agg tgc cag ctc aaa 424  
Phe Tyr Val Leu Arg Gln Arg Ile Ala Arg Ile Arg Cys Gln Leu Lys  
60 65 70

gct gtg tgc caa cca cga tgc aaa cat ggt gaa tgt atc ggg cca aac 472  
Ala Val Cys Gln Pro Arg Cys Lys His Gly Glu Cys Ile Gly Pro Asn  
75 80 85 90

aag tgc aag tgt cat cct ggt tat gct gga aaa acc tgt aat caa gcc 520  
Lys Cys Lys Cys His Pro Gly Tyr Ala Gly Lys Thr Cys Asn Gln Ala  
95 100 105

gta ggt ttt gaa aga tgt atg gtt cca gcc ggg cgc cgt ggc tct acc 568  
Val Gly Phe Glu Arg Cys Met Val Pro Ala Gly Arg Arg Gly Ser Thr  
110 115 120

ctg taatccacg acttggaaag gccgaggcg cgccatcacg aggtcaggat 621  
Leu

atcgagacca tcctggctaa cacggtaaa ccccatctc actaaaaata caaaaaaaaaa 681  
aaaaaaaaaaa 691

<210> 32  
<211> 123  
<212> PRT  
<213> Homo sapiens

<400> 32  
Met Asp Phe Leu Leu Ala Leu Val Leu Val Ser Ser Leu Tyr Leu Gln  
1 5 10 15

Ala Ala Ala Glu Tyr Asp Gly Arg Trp Pro Arg Gln Ile Val Ser Ser  
20 25 30

Ile Gly Leu Cys Arg Tyr Gly Gly Arg Ile Asp Cys Cys Trp Gly Trp  
35 40 45

Ala Arg Gln Ser Trp Gly Gln Cys Gln Pro Phe Tyr Val Leu Arg Gln  
50 55 60

Arg Ile Ala Arg Ile Arg Cys Gln Leu Lys Ala Val Cys Gln Pro Arg  
65 70 75 80

Cys Lys His Gly Glu Cys Ile Gly Pro Asn Lys Cys Lys Cys His Pro  
85 90 95

Gly Tyr Ala Gly Lys Thr Cys Asn Gln Ala Val Gly Phe Glu Arg Cys  
100 105 110

Met Val Pro Ala Gly Arg Arg Gly Ser Thr Leu

115

120

<210> 33  
<211> 2112  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (203)..(1948)

<400> 33  
ggggggggc tccgggcgcc gcgcagcaga cctgctccgg ccgcgcgcct cgccgctgtc 60  
ctccgggagc ggcagcaga gccccggcg cgagggtctgg gggttctcg agactcttag 120  
aggggcccct cccatggcg cccaccaccc caacctgttc ctgcgcgcct actgcgcgtc 180  
gccccaggac ccgctgcca ac atg gat ttt ctc ctg gcg ctg gtg ctg gta 232  
Met Asp Phe Leu Leu Ala Leu Val Leu Val  
1 5 10

tcc tcg ctc tac ctg cag gcg gcc gag ttc gac ggg agg tgg ccc 280  
Ser Ser Leu Tyr Leu Gln Ala Ala Ala Glu Phe Asp Gly Arg Trp Pro  
15 20 25

agg caa ata gtg tca tcg att ggc cta tgt cgt tat ggt ggg agg att 328  
Arg Gln Ile Val Ser Ser Ile Gly Leu Cys Arg Tyr Gly Arg Ile  
30 35 40

gac tgc tgc tgg ggc tgg gct cgc cag tct tgg gga cag tgt cag cct 376  
Asp Cys Cys Trp Gly Trp Ala Arg Gln Ser Trp Gly Gln Cys Gln Pro  
45 50 55

ttc tac gtc tta agg cag aga ata gcc agg ata agg tgc cag ctc aaa 424  
Phe Tyr Val Leu Arg Gln Arg Ile Ala Arg Ile Arg Cys Gln Leu Lys  
60 65 70

gct gtg tgc caa cca cga tgc aaa cat ggt gaa tgt atc ggg cca aac 472  
Ala Val Cys Gln Pro Arg Cys Lys His Gly Glu Cys Ile Gly Pro Asn  
75 80 85 90

aag tgc aag tgt cat cct ggt tat gct gga aaa acc tgt att caa gtt 520  
Lys Cys Lys Cys His Pro Gly Tyr Ala Gly Lys Thr Cys Ile Gln Val  
95 100 105

tta aat gag tgt ggc ctg aag ccc cgg ccc tgt aag cac agg tgc atg 568  
Leu Asn Glu Cys Gly Leu Lys Pro Arg Pro Cys Lys His Arg Cys Met  
110 115 120

aac act tac ggc agc tac aag tgc tac tgt ctc aac gga tat atg ctc 616

Asn Thr Tyr Gly Ser Tyr Lys Cys Tyr Cys Leu Asn Gly Tyr Met Leu  
125                130                135

atg ccg gat ggt tcc tgc tca agt gcc ctg acc tgc tcc atg gca aac 664  
Met Pro Asp Gly Ser Cys Ser Ser Ala Leu Thr Cys Ser Met Ala Asn  
140                145                150

tgt cag tat ggc tgt gat gtt gtt aaa gga caa ata cgg tgc cag tgc 712  
Cys Gln Tyr Gly Cys Asp Val Val Lys Gly Gln Ile Arg Cys Gln Cys  
155                160                165                170

cca tcc cct ggc ctg cag ctg gct gat ggg agg acc tgt gta gat 760  
Pro Ser Pro Gly Leu Gln Leu Ala Pro Asp Gly Arg Thr Cys Val Asp  
175                180                185

gtt gat gaa tgt gct aca gga aga gcc tcc tgc cct aga ttt agg caa 808  
Val Asp Glu Cys Ala Thr Gly Arg Ala Ser Cys Pro Arg Phe Arg Gln  
190                195                200

tgt gtc aac act ttt ggg agc tac atc tgc aag tgt cat aaa ggc ttc 856  
Cys Val Asn Thr Phe Gly Ser Tyr Ile Cys Lys Cys His Lys Gly Phe  
205                210                215

gat ctc atg tat att gga ggc aaa tat caa tgt cat gac ata gac gaa 904  
Asp Leu Met Tyr Ile Gly Gly Lys Tyr Gln Cys His Asp Ile Asp Glu  
220                225                230

tgc tca ctt ggt cag tat cag tgc agc agc ttt gct cga tgt tat aac 952  
Cys Ser Leu Gly Gln Tyr Gln Cys Ser Ser Phe Ala Arg Cys Tyr Asn  
235                240                245                250

gta cgt ggg tcc tac aag tgc aaa tgt aaa gaa gga tac cag ggt gat 1000  
Val Arg Gly Ser Tyr Lys Cys Lys Cys Lys Glu Gly Tyr Gln Gly Asp  
255                260                265

gga ctg act tgt gtg tat atc cca aaa gtt atg att gaa cct tca ggt 1048  
Gly Leu Thr Cys Val Tyr Ile Pro Lys Val Met Ile Glu Pro Ser Gly  
270                275                280

cca att cat gta cca aag gga aat ggt acc att tta aag ggt gac aca 1096  
Pro Ile His Val Pro Lys Gly Asn Gly Thr Ile Leu Lys Gly Asp Thr  
285                290                295

gga aat aat aat tgg att cct gat gtt gga agt act tgg tgg cct ccg 1144  
Gly Asn Asn Asn Trp Ile Pro Asp Val Gly Ser Thr Trp Trp Pro Pro  
300                305                310

aag aca cca tat att cct cct atc att acc aac agg cct act tct aag 1192  
Lys Thr Pro Tyr Ile Pro Pro Ile Thr Asn Arg Pro Thr Ser Lys  
315                320                325                330

cca aca aca aga cct aca cca aag cca aca cca att cct act cca cca 1240  
Pro Thr Thr Arg Pro Thr Pro Lys Pro Thr Pro Ile Pro Thr Pro Pro

335            340            345

cca cca cca ccc ctg cca aca gag ctc aga aca aca cct cta cca cct aca 1288  
Pro Pro Pro Pro Leu Pro Thr Glu Leu Arg Thr Pro Leu Pro Pro Thr  
350            355            360

acc cca gaa agg cca acc acc gga ctg aca act ata gca cca gct gcc 1336  
Thr Pro Glu Arg Pro Thr Thr Gly Leu Thr Thr Ile Ala Pro Ala Ala  
365            370            375

agt aca cct cca gga ggg att aca gtt gac aac agg gta cag aca gac 1384  
Ser Thr Pro Pro Gly Gly Ile Thr Val Asp Asn Arg Val Gln Thr Asp  
380            385            390

cct cag aaa ccc aga gga gat gtg ttc att cca cg<sup>g</sup> caa cct tca aat 1432  
Pro Gln Lys Pro Arg Gly Asp Val Phe Ile Pro Arg Gln Pro Ser Asn  
395            400            405            410

gac ttg ttt gaa ata ttt gaa ata gaa aga gga gtc agt gca gac gat 1480  
Asp Leu Phe Glu Ile Phe Glu Ile Glu Arg Gly Val Ser Ala Asp Asp  
415            420            425

gaa gca aag gat gat cca ggt gtt ctg gta cac agt tgt aat ttt gac 1528  
Glu Ala Lys Asp Asp Pro Gly Val Leu Val His Ser Cys Asn Phe Asp  
430            435            440

cat gga ctt tgt gga tgg atc agg gag aaa gac aat gac ttg cac tgg 1576  
His Gly Leu Cys Gly Trp Ile Arg Glu Lys Asp Asn Asp Leu His Trp  
445            450            455

gaa cca atc agg gac cca gca ggt gga caa tat ctg aca gtc tcg gca 1624  
Glu Pro Ile Arg Asp Pro Ala Gly Gly Gln Tyr Leu Thr Val Ser Ala  
460            465            470

gcc aaa gcc cca ggg gga aaa gct gca cgc ttg gtg cta cct ctc ggc 1672  
Ala Lys Ala Pro Gly Gly Lys Ala Ala Arg Leu Val Leu Pro Leu Gly  
475            480            485            490

cgc ctt atg cat tca ggg gac ctg tgc ctg tca ttc agg cac aag gtg 1720  
Arg Leu Met His Ser Gly Asp Leu Cys Leu Ser Phe Arg His Lys Val  
495            500            505

acg ggg ctg cac tct ggc aca ctc cag gtg ttt gtg aga aaa cac ggt 1768  
Thr Gly Leu His Ser Gly Thr Leu Gln Val Phe Val Arg Lys His Gly  
510            515            520

gcc cac gga gca gcc ctg tgg gga aga aat ggt ggc cat ggc tgg agg 1816  
Ala His Gly Ala Ala Leu Trp Gly Arg Asn Gly Gly His Gly Trp Arg  
525            530            535

caa aca cag atc acc ttg cga ggg gct gac atc aag agc gtc gtc ttc 1864  
Gln Thr Gln Ile Thr Leu Arg Gly Ala Asp Ile Lys Ser Val Val Phe  
540            545            550

aaa ggt gaa aaa agg cgt ggt cac act ggg gag att gga tta gat gat 1912  
Lys Gly Glu Lys Arg Arg Gly His Thr Gly Glu Ile Gly Leu Asp Asp

555 560 565 570

gtg agc ttg aaa aaa ggc cac tgc tct gaa gaa cgc taacaactcc 1958  
Val Ser Leu Lys Lys Gly His Cys Ser Glu Glu Arg  
575 580

agaactaaca atgaactcct atgttgctct atccctttt tccaattctc atcttctctc 2018

ctcttcctcc ttttatcagg cctaggagaa gagtgggtca gtgggtcaga aggaagtcta 2078

tttgtgacc caggttcttc tggcctgctt ttgt 2112

<210> 34

<211> 582

<212> PRT

<213> Homo sapiens

<400> 34

Met Asp Phe Leu Leu Ala Leu Val Leu Val Ser Ser Leu Tyr Leu Gln  
1 5 10 15

Ala Ala Ala Glu Phe Asp Gly Arg Trp Pro Arg Gln Ile Val Ser Ser  
20 25 30

Ile Gly Leu Cys Arg Tyr Gly Gly Arg Ile Asp Cys Cys Trp Gly Trp  
35 40 45

Ala Arg Gln Ser Trp Gly Gln Cys Gln Pro Phe Tyr Val Leu Arg Gln  
50 55 60

Arg Ile Ala Arg Ile Arg Cys Gln Leu Lys Ala Val Cys Gln Pro Arg  
65 70 75 80

Cys Lys His Gly Glu Cys Ile Gly Pro Asn Lys Cys Lys Cys His Pro  
85 90 95

Gly Tyr Ala Gly Lys Thr Cys Ile Gln Val Leu Asn Glu Cys Gly Leu  
100 105 110

Lys Pro Arg Pro Cys Lys His Arg Cys Met Asn Thr Tyr Gly Ser Tyr  
115 120 125

Lys Cys Tyr Cys Leu Asn Gly Tyr Met Leu Met Pro Asp Gly Ser Cys  
130 135 140

Ser Ser Ala Leu Thr Cys Ser Met Ala Asn Cys Gln Tyr Gly Cys Asp  
145 150 155 160

Val Val Lys Gly Gln Ile Arg Cys Gln Cys Pro Ser Pro Gly Leu Gln

165                  170                  175  
Leu Ala Pro Asp Gly Arg Thr Cys Val Asp Val Asp Glu Cys Ala Thr  
180                  185                  190  
Gly Arg Ala Ser Cys Pro Arg Phe Arg Gln Cys Val Asn Thr Phe Gly  
195                  200                  205  
Ser Tyr Ile Cys Lys Cys His Lys Gly Phe Asp Leu Met Tyr Ile Gly  
210                  215                  220  
Gly Lys Tyr Gln Cys His Asp Ile Asp Glu Cys Ser Leu Gly Gln Tyr  
225                  230                  235                  240  
Gln Cys Ser Ser Phe Ala Arg Cys Tyr Asn Val Arg Gly Ser Tyr Lys  
245                  250                  255  
Cys Lys Cys Lys Glu Gly Tyr Gln Gly Asp Gly Leu Thr Cys Val Tyr  
260                  265                  270  
Ile Pro Lys Val Met Ile Glu Pro Ser Gly Pro Ile His Val Pro Lys  
275                  280                  285  
Gly Asn Gly Thr Ile Leu Lys Gly Asp Thr Gly Asn Asn Asn Trp Ile  
290                  295                  300  
Pro Asp Val Gly Ser Thr Trp Trp Pro Pro Lys Thr Pro Tyr Ile Pro  
305                  310                  315                  320  
Pro Ile Ile Thr Asn Arg Pro Thr Ser Lys Pro Thr Thr Arg Pro Thr  
325                  330                  335  
Pro Lys Pro Thr Pro Ile Pro Thr Pro Pro Pro Pro Pro Leu Pro  
340                  345                  350  
Thr Glu Leu Arg Thr Pro Leu Pro Pro Thr Thr Pro Glu Arg Pro Thr  
355                  360                  365  
Thr Gly Leu Thr Thr Ile Ala Pro Ala Ala Ser Thr Pro Pro Gly Gly  
370                  375                  380  
Ile Thr Val Asp Asn Arg Val Gln Thr Asp Pro Gln Lys Pro Arg Gly  
385                  390                  395                  400  
Asp Val Phe Ile Pro Arg Gln Pro Ser Asn Asp Leu Phe Glu Ile Phe  
405                  410                  415  
Glu Ile Glu Arg Gly Val Ser Ala Asp Asp Glu Ala Lys Asp Asp Pro  
420                  425                  430  
Gly Val Leu Val His Ser Cys Asn Phe Asp His Gly Leu Cys Gly Trp  
435                  440                  445

Ile Arg Glu Lys Asp Asn Asp Leu His Trp Glu Pro Ile Arg Asp Pro  
450                455                460

Ala Gly Gly Gln Tyr Leu Thr Val Ser Ala Ala Lys Ala Pro Gly Gly  
465                470                475                480

Lys Ala Ala Arg Leu Val Leu Pro Leu Gly Arg Leu Met His Ser Gly  
485                490                495

Asp Leu Cys Leu Ser Phe Arg His Lys Val Thr Gly Leu His Ser Gly  
500                505                510

Thr Leu Gln Val Phe Val Arg Lys His Gly Ala His Gly Ala Ala Leu  
515                520                525

Trp Gly Arg Asn Gly Gly His Gly Trp Arg Gln Thr Gln Ile Thr Leu  
530                535                540

Arg Gly Ala Asp Ile Lys Ser Val Val Phe Lys Gly Glu Lys Arg Arg  
545                550                555                560

Gly His Thr Gly Glu Ile Gly Leu Asp Asp Val Ser Leu Lys Lys Gly  
565                570                575

His Cys Ser Glu Glu Arg  
580

<210> 35  
<211> 34  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR PRIMER

<400> 35  
gaattctgc caagagagta cacagtatt aatg                34

<210> 36  
<211> 34  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR PRIMER

<400> 36  
aagctttgc caagagagta cacagtatt aatg                34

<210> 37  
<211> 30  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR PRIMER

<400> 37  
ctcgagttc atattctt caatccagtc 30

<210> 38  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR PRIMER

<400> 38  
tgtggccagg ttctgcga 18

<210> 39  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR PRIMER

<400> 39  
cttgacaagg ctggatct 18

<210> 40  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR PRIMER

<400> 40  
cctaccaaga agccagcc 18

<210> 41  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR PRIMER

<400> 41  
tcgcagaacc tggccaca 18

<210> 42  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR PRIMER

<400> 42  
agatccagcc ttgtcaag 18

<210> 43  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR PRIMER

<400> 43  
ggctggcttc ttggtagg 18

<210> 44  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR PRIMER

<400> 44  
caggcagcca tctacaggag g 21

<210> 45  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR PRIMER

<400> 45  
cctcctgttag atggctgcct g 21

<210> 46  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR PRIMER

<400> 46  
caggagtccc acatcact 18

<210> 47  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR PRIMER

<400> 47  
agtgatgtgg gactcctg 18

<210> 48  
<211> 38  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR PRIMER

<400> 48  
gctagccacc atggagctgg gttgctggac gcagttgg 38

<210> 49  
<211> 35  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR PRIMER

<400> 49  
aggacgtgga gtgaggatcc tatgctctgg atagg 35

<210> 50  
<211> 30  
<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR PRIMER

<400> 50

ctcgtcctcg aggtaagcc tatccctaac

30

<210> 51

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR PRIMER

<400> 51

ctcgtcgccc cctgatcag cgggtttaaa c

31

<210> 52

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR PRIMER

<400> 52

ggatccaaat cctgtccatc tgtgtgtcgc tg

32

<210> 53

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR PRIMER

<400> 53

ctcgagagcc aaaggtaaat tggggtttt gtaag

35

<210> 54

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR PRIMER

<400> 54  
cgagacagca actatctc 18

<210> 55  
<211> 18  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Description of Artificial Sequence: PCR PRIMER

<400> 55  
cgactggata tgtccaat 18

<210> 56  
<211> 18  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Description of Artificial Sequence: PCR PRIMER

<400> 56  
acaattactg tgaagtct 18

<210> 57  
<211> 18  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Description of Artificial Sequence: PCR PRIMER

<400> 57  
gagatagttt ctgtctcg 18

<210> 58  
<211> 18  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Description of Artificial Sequence: PCR PRIMER

<400> 58  
atggacata tccagtcg 18

<210> 59

<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR PRIMER

<400> 59  
agacttcaca gtaattgt 18

<210> 60  
<211> 34  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR PRIMER

<400> 60  
ggatccgagg ctgaaggcaa tgcaagctgc acag 34

<210> 61  
<211> 33  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR PRIMER

<400> 61  
tcgagcagtg gaatgttaggt gctgtgaatg cag 33

<210> 62  
<211> 33  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR PRIMER

<400> 62  
ggatccgcgg tcctgtggaa gcatgtgcgg ctg 33

<210> 63  
<211> 30  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR PRIMER

<400> 63

ctcgagcgtg ttgcacacca gcacatctgc

30

<210> 64

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR PRIMER

<400> 64

gacgtggccc tcatcgccaa c

21

<210> 65

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR PRIMER

<400> 65

ctaggcgagg agtacattct g

21

<210> 66

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR PRIMER

<400> 66

ctggaccggg ctgagcaa

18

<210> 67

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR PRIMER

<400> 67

gttggcgatg agggccacgt c

21

<210> 68  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR PRIMER

<400> 68  
cagaatgtac tcctcgcc ta g 21

<210> 69  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR PRIMER

<400> 69  
ttgctcagcc cggtccag 18

<210> 70  
<211> 33  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR PRIMER

<400> 70  
ggtacctgtg gagagactcc agagcaaata cga 33

<210> 71  
<211> 33  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR PRIMER

<400> 71  
ctcgagagtg atgactcttg taggcacgt tac 33

<210> 72  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR PRIMER  
  
<400> 72  
gcttgtatc agtttcgt 18  
  
<210> 73  
<211> 18  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Description of Artificial Sequence: PCR PRIMER  
  
<400> 73  
tgcaccctggt taatagac 18  
  
<210> 74  
<211> 18  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Description of Artificial Sequence: PCR PRIMER  
  
<400> 74  
actgagcagc agcgttgt 18  
  
<210> 75  
<211> 18  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Description of Artificial Sequence: PCR PRIMER  
  
<400> 75  
acgaaactga tcacaagg 18  
  
<210> 76  
<211> 18  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Description of Artificial Sequence: PCR PRIMER  
  
<400> 76

tattaaccag gtgcaatt

18

<210> 77  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR PRIMER

<400> 77  
acaacgctgc tgctcagt

18

<210> 78  
<211> 30  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR PRIMER

<400> 78  
ggatccgagt acgacgggag gtggccagg

30

<210> 79  
<211> 36  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR PRIMER

<400> 79  
ctcgagcagg gtagagccac ggcccccggc tggaac

36

<210> 80  
<211> 261  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: AMPLIFICATION  
PRODUCT 16467945.0.85-S259.A

<400> 80  
gagtacgacg ggaggtggcc caggcaaata gtgtcatcga ttggcctatg tcgttatgg 60  
gggaggattg actgctgctg gggctggctt cgccagtctt ggggacagtg tcagctgtg 120  
tgccaaccac gatgcaaaca tggtaatgt atcggggcaa acaagtcaa gtgtcatct 180  
ggttatgctg gaaaaacctg taatcaagcc gtaggttttg aaagatgtat ggttccagcc 240

gggcgccgtg gctctaccct g

261

<210> 81

<211> 1638

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: CONSTRUCT

16467945.0.88-S261.D NUCLEIC ACID

<400> 81

gagttcgcacg ggagggtggcc caggcaataa gtgtcatcga ttggcctatg tcgttatgt 60  
gggaggattg actgctgtg gggctgggt cgccagtctt ggggacagtg tcagcctgt 120  
tgccaaaccac gatgcaaaca tggtaatgt atcggccaa acaagtgca gtgtcatcct 180  
ggttatgtg gaaaaacctg tattcaagg ttaaatgagt gtggcctgaa gccccggccc 240  
tgtaagcaca ggtgcgtgaa cacttacggc agctacaagt gctactgtct caacggat 300  
atgctcatgc cggatgggtc ctgctcaagt gcccgtacct gctccatggc aaactgtcag 360  
tatggctgtg atgtgttaa aggacaaata cggtgccagt gcccattcccc tggcctgcag 420  
ctggctctg atgggaggac ctgtgttagat gtgtatgaa gtgtacagg aagaggctcc 480  
tgcccttagat ttaggcaatg tgtcaacact ttggggact acatctgca gtgtataaa 540  
ggcttcgatc tcatgtat tggaggcaaa tatcaatgtc atgacataga cgaatgtca 600  
cttggtcagt atcagtgcag cagcttgcg cgtatgtata acgtacgtgg gtcctacaag 660  
tgcaaatgtt aagaaggata ccagggtgt ggactgactt gtgtatataa cccaaaagt 720  
atgattgaac cttcagggtcc aattcatgtt ccaaaggaaa atggatccat tttaaagggt 780  
gacacaggaa ataataattt gattctgtat gtgttggactt ctgggtggcc tccgaagaca 840  
ccatatattt ctcctatcat taccacacgg cctacttcta agccaacaac aagacctaca 900  
ccaaagccaa caccaatttcc tactccacca ccaccaccc cctgcacac agagctcaga 960  
acacccctcac cacctacaac cccagaaaagg ccaaccacccg gactgacaac tatagcacca 1020  
gctgccagta cacccctcagg agggattaca gtgtacaaca gggtaacac agacccttag 1080  
aaacccctcagg gagatgtgtt cattccacgg caacccttcaa atgacttgtt tgaaatattt 1140  
gaaatagaaaa gaggagtccat tgccatgtt gaaaggaaagg atgatccagg tttctggta 1200  
cacagtgtt attttgacca tggactttgtt ggttggatca gggagaagaaga caatgactt 1260  
caactggaaac caatcaggaa cccagccagg ggacaatatc tgacagtgtc ggcaggccaa 1320  
gccccagggg gaaaaggctgc acgcttgggt ctacctctcg gccccttat gcattcagg 1380  
gacctgtgcc tgcatttcag gcacaagggt acggggctgc actctggcac actccagg 1440  
tttgtgaaac aacacgggtcc acacggagca gcccctgggg gaagaaatgg tggccatggc 1500  
tggaggcaaa cacagatcac ctgcggagg gctgacatca agagcgtgtt ctcaaggt 1560  
gaaaaaaaggc gtggtcacac tggggagatt ggatttagatg atgtgagctt gaaaaaaaggc 1620  
caactgctgtg aagaacgc 1638

<210> 82

<211> 546

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: TRANSLATION

FROM AMPLIFICATION PRODUCT 16467945.0.88-S261.D

<400> 82

Glu Tyr Asp Gly Arg Trp Pro Arg Gln Ile Val Ser Ser Ile Gly Leu  
1 5 10 15

Cys Arg Tyr Gly Gly Arg Ile Asp Cys Cys Trp Gly Trp Ala Arg Gln  
20 25 30

Ser Trp Gly Gln Cys Gln Pro Val Cys Gln Pro Arg Cys Lys His Gly  
35 40 45

Glu Cys Ile Gly Pro Asn Lys Cys Lys Cys His Pro Gly Tyr Ala Gly  
50 55 60

Lys Thr Cys Ile Gln Val Leu Asn Glu Cys Gly Leu Lys Pro Arg Pro  
65 70 75 80

Cys Lys His Arg Cys Met Asn Thr Tyr Gly Ser Tyr Lys Cys Tyr Cys  
85 90 95

Leu Asn Gly Tyr Met Leu Met Pro Asp Gly Ser Cys Ser Ser Ala Leu  
100 105 110

Thr Cys Ser Met Ala Asn Cys Gln Tyr Gly Cys Asp Val Val Lys Gly  
115 120 125

Gln Ile Arg Cys Gln Cys Pro Ser Pro Gly Leu Gln Leu Ala Pro Asp  
130 135 140

Gly Arg Thr Cys Val Asp Val Asp Glu Cys Ala Thr Gly Arg Ala Ser  
145 150 155 160

Cys Pro Arg Phe Arg Gln Cys Val Asn Thr Phe Gly Ser Tyr Ile Cys  
165 170 175

Lys Cys His Lys Gly Phe Asp Leu Met Tyr Ile Gly Gly Lys Tyr Gln  
180 185 190

Cys His Asp Ile Asp Glu Cys Ser Leu Gly Gln Tyr Gln Cys Ser Ser  
195 200 205

Phe Ala Arg Cys Tyr Asn Val Arg Gly Ser Tyr Lys Cys Lys Cys Lys  
210 215 220

Glu Gly Tyr Gln Gly Asp Gly Leu Thr Cys Val Tyr Ile Pro Lys Val  
225 230 235 240

Met Ile Glu Pro Ser Gly Pro Ile His Val Pro Lys Gly Asn Gly Thr  
245 250 255

Ile Leu Lys Gly Asp Thr Gly Asn Asn Asn Trp Ile Pro Asp Val Gly  
260 265 270

Ser Thr Trp Trp Pro Pro Lys Thr Pro Tyr Ile Pro Pro Ile Ile Thr  
275 280 285

Asn Arg Pro Thr Ser Lys Pro Thr Thr Arg Pro Thr Pro Lys Pro Thr  
290                295                300

Pro Ile Pro Thr Pro Pro Pro Pro Leu Pro Thr Glu Leu Arg  
305                310                315                320

Thr Pro Leu Pro Pro Thr Thr Pro Glu Arg Pro Thr Thr Gly Leu Thr  
325                330                335

Thr Ile Ala Pro Ala Ala Ser Thr Pro Pro Gly Gly Ile Thr Val Asp  
340                345                350

Asn Arg Val Gln Thr Asp Pro Gln Lys Pro Arg Gly Asp Val Phe Ile  
355                360                365

Pro Arg Gln Pro Ser Asn Asp Leu Phe Glu Ile Phe Glu Ile Glu Arg  
370                375                380

Gly Val Ser Ala Asp Asp Glu Ala Lys Asp Asp Pro Gly Val Leu Val  
385                390                395                400

His Ser Cys Asn Phe Asp His Gly Leu Cys Gly Trp Ile Arg Glu Lys  
405                410                415

Asp Asn Asp Leu His Trp Glu Pro Ile Arg Asp Pro Ala Gly Gly Gln  
420                425                430

Tyr Leu Thr Val Ser Ala Ala Lys Ala Pro Gly Gly Lys Ala Ala Arg  
435                440                445

Leu Val Leu Pro Leu Gly Arg Leu Met His Ser Gly Asp Leu Cys Leu  
450                455                460

Ser Phe Arg His Lys Val Thr Gly Leu His Ser Gly Thr Leu Gln Val  
465                470                475                480

Phe Val Arg Lys His Gly Ala His Gly Ala Ala Leu Trp Gly Arg Asn  
485                490                495

Gly Gly His Gly Trp Arg Gln Thr Gln Ile Thr Leu Arg Gly Ala Asp  
500                505                510

Ile Lys Ser Val Val Phe Lys Gly Glu Lys Arg Arg Gly His Thr Gly  
515                520                525

Glu Ile Gly Leu Asp Asp Val Ser Leu Lys Lys Gly His Cys Ser Glu  
530                535                540

Glu Arg  
545

<210> 83  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR PRIMER

<400> 83  
cagtcaatgg gtaccagaaaa ataaca 26

<210> 84  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PROBE

<400> 84  
cctgggctta tcaacggacg cca 23

<210> 85  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR PRIMER

<400> 85  
accacgggtgc caatttttagc 20

<210> 86  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR PRIMER

<400> 86  
gctaaatcct gtccatctgt gt 22

<210> 87  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PROBE

<400> 87  
tgaaacccgc atcgacgca

20

<210> 88  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR PRIMER

<400> 88  
atggatgtca gaaagcgatc a

21

<210> 89  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR PRIMER

<400> 89  
cagtacaca gctgcttat tctca

25

<210> 90  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PROBE

<400> 90  
aatctaccc ttgcgtggc tggaac

26

<210> 91  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR PRIMER

<400> 91  
ggacacctcc agggaaacgt

20

<210> 92  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR PRIMER

<400> 92  
cctgcaaagc cgtgaggt 18

<210> 93  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PROBE

<400> 93  
acggcatctc tggccgga acc 23

<210> 94  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR PRIMER

<400> 94  
ggtgtccctgg tagattcgga ag 22

<210> 95  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR PRIMER

<400> 95  
gtactgccgc cagcttacct 20

<210> 96  
<211> 28  
<212> DNA

<213> Artificial Sequence  
<220>  
<223> Description of Artificial Sequence: PROBE  
<400> 96  
cacagagcca gcagtgcacat atgacaaa 28

<210> 97  
<211> 24  
<212> DNA  
<213> Artificial Sequence  
<220>  
<223> Description of Artificial Sequence: PCR PRIMER  
<400> 97  
gacatggctt tcgtaaataa tgca 24

<210> 98  
<211> 17  
<212> DNA  
<213> Artificial Sequence  
<220>  
<223> Description of Artificial Sequence: PCR PRIMER  
<400> 98  
cgcccctaca accgcat 17

<210> 99  
<211> 33  
<212> DNA  
<213> Artificial Sequence  
<220>  
<223> Description of Artificial Sequence: PROBE  
<400> 99  
ccatagagtc agcgttgac aatccaaactt acg 33

<210> 100  
<211> 23  
<212> DNA  
<213> Artificial Sequence  
<220>  
<223> Description of Artificial Sequence: PCR PRIMER

<400> 100  
ctgcaaagga aagagatcca gtc 23

<210> 101  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR PRIMER

<400> 101  
ttggcctgga ctgcttc 20

<210> 102  
<211> 28  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PROBE

<400> 102  
catctctgtc taccctggct atggcgty 28

<210> 103  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR PRIMER

<400> 103  
aggctgatat tctggacatt gatt 24

<210> 104  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR PRIMER

<400> 104  
ccaagttagat gggttctgtt tgc 23

<210> 105

<211> 28  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PROBE

<400> 105  
cccagttacc tccacagggt atttccca 28

<210> 106  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR PRIMER

<400> 106  
cgacgctgct gctcagtata ac 22

<210> 107  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR PRIMER

<400> 107  
ccacctacaa cccccagaaag g 21

<210> 108  
<211> 30  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PROBE

<400> 108  
caaccaccgg actgacaact atagcaccag 30

<210> 109  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR PRIMER

<400> 109

tgtaatccct cctggagggt tac

23

<210> 110

<211> 87

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: TRANSLATION  
FROM AMPLIFICATION PRODUCT 16467945.0.85-S259.A

<400> 110

Glu Tyr Asp Gly Arg Trp Pro Arg Gln Ile Val Ser Ser Ile Gly Leu  
1 5 10 15

Cys Arg Tyr Gly Gly Arg Ile Asp Cys Cys Trp Gly Trp Ala Arg Gln  
20 25 30

Ser Trp Gly Gln Cys Gln Pro Val Cys Gln Pro Arg Cys Lys His Gly  
35 40 45

Glu Cys Ile Gly Pro Asn Lys Cys Lys Cys His Pro Gly Tyr Ala Gly  
50 55 60

Lys Thr Cys Asn Gln Ala Val Gly Phe Glu Arg Cys Met Val Pro Ala  
65 70 75 80

Gly Arg Arg Gly Ser Thr Leu  
85